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RESULT 4
AAW97408
ID AAW97408
ID AAW97408
ID AAW97408
AC AAW9
AC Lytl
XXX magg
KW magg
KW magg
KW magg
KW magg
II-I
XXX JI-I
XXX JI-I
XXX JI-I
XXX JI-I
XXX JI-I
XXX II-I
AXX 
RESULT 5
AAW99125
ID AAW9
XX
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                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                  AAW99125 standard;
                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an lytic peptide which is used in the course of the inventin to produce transgenic poinsettia plants with increased resistance to pathogens. The specification describes methods for the in vitro regeneration of Poinsettia. Transgenic Poinsettia can now be produced with e.g. increased resistance to pathogens or insects, controllable flower colour, modified habit (more compact form, earlier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      In vitro regeneration of Poinsettia - us containing casein hydrolysate, used to previate, e.g. increased disease resistance, altered habit and flowering time
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 51; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX16060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-153796/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09906566-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   magainin; transgenic;
resistance; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lytic peptide magainin 2*S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW97408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97408 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                              flowering)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SANF-) SANFORD SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eck J;
                                                                                                                                  16
                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KWKLFKKIGIGKFLHSAK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                  MGIGKFLHSAKKF 28
                                                                                                                                                                               IGIGKFLHSAKKF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KWKLFKKIGIGAVLKVLK 18
                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                                                                                              and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chou
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                   Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0903944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US15917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                              increased resistance
                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 39 AA.
                                                                                                                                                                                                                                               59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.3%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eisenreich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .poinsettia; in vitro regeneration;
flower colour.
                     39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                               Score 64; DB 20;
Pred. No. 0.0071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; Depred. No. 0.
                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sanford
                                                                                                                                                                                                                                                                                                                                                            to ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             using embryo-induction medium produce transgenic plants e, controllable flower colour,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                  Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 32;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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CA2228730-A1

Unidentified

Antimicrobial; styelin; microbial degradation; bactericide; fungicide; plant protection; styelin A; magainin 2.

viricide;

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RESULT 6
AAY67472
ID AAY6
XX AAY6
AC AAY6
XX 12-A
DT 12-A
XX Mag:
XX Ant:
KW Ant:
KW fun:
XX GS Uni
XX UA2
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                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an antimicrobial peptide. The present invention also describes a method of conferring microbial resistance on a plant cell comprising transforming the cell to express two peptides selected from the magainin and PGL classes, where the peptides are separately compartmentalised. The antimicrobial peptide is effective against phytopathogenic microbes including bacteria, fungi, and phytoplasma. It can also be used to target other plant pests, such as nematodes and viruses. The nucleic acid sequence encoding the peptide can be used to transform plants to provide antimicrobial resistance. The method is especially useful in preventing powdery mildew. The method allows for levels of peptide expression to provide resistance to phytopathogenic microbes without otherwise affecting the plant cells.
                                                                                                                                                 AAY67472;
                                                                                                                          12-MAY-2000
                                                                                                                                                                          AAY67472 standard;
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antimicrobial peptides - comprising magainin and PGL classes peptides having an N-terminal methionine, used particularly for providing resistance in plants to pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial peptide; powdery mildew.
                                                                                              Magainin 2 partial peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 40; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANF-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW99125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-153794/13.
DB; AAX19274.
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                                                                                                                                                                                                                                                                                     . Similarity 92.3
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SANFORD SCI INC
                                                                                                                                                                                                                                        MGIGKFLHSAKKF
                                                                                                                                                                                                                                                     IGIGKFLHSAKKF
                                                                                                                                                                                                                                                                                                                                         39 AA;
                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   localised antimicrobial magainin 2 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0054315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US16032
                                                                                                                                                                         peptide;
                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                   59.3%;
                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith
                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                     Score 64; DB
Pred. No. 0.00
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Eck
                                                                                                                                                                                                                                                                                                DB 20;
0.0071;
                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                            Length 39
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic plant;
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                                                                                                                                                                                                                                                                                     Gaps
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RESULT
AAP7120
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antimicrobial peptides (styelins) (and acetylated forms, salts, amides and esters of styelins), isolated from Styela clava and characterized by specific patterns of basic and hydrophobic amino acid side chains which display a broad spectrum of antimicrobial activities. The peptides are of a specified formula and display a wide range of antimicrobial activities and are therefore useful for preserving materials susceptible to microbial degradation, for protecting plants against bacterial infection and in the therapeutic and prophylactic protection of animals against bacteria, fungi and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial styelin peptides isolated from Styela clava useful preserving materials vulnerable to microbial degradation and for protecting plants and animals against pathogenic microbes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao
                                                                      04-MAR-1987;
                                                                                                                                                                synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1998;
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WPI;
                                                                                                                    08-SEP-1987
                                                                                                                                          USN7021493-N
                                                                                                                                                                                         Magainin;
                                                                                                                                                                                                                                       17-DEC-2001
01-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
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20-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1999
                      Zasloff MA;
                                             (USSH ) US DEPT
                                                                                            04-MAR-1987;
                                                                                                                                                                                                               Magainin III polypeptide
                                                                                                                                                                                                                                                                           AAP71208;
                                                                                                                                                                                                                                                                                                  AAP71208 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e compounds may also be used as standards in antimicrobial assays and affinity ligands for absorption of counterpart structures in microbes. cluding viruses. The present sequence represents a partial fragment of gainin 2, used in comparison studies.
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1987-334845/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                                                                                                                                                                                                                                                                           GIGKFLHSAKKF 12
                                                                                                                                                                                                                                                                                                                                                                                  GIGKFLHSAKKF 20
                                                                                                                                                                                         antimicrobial; antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ţ,
                                                                                                                                                                                                                                       (updated)
(first entry)
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98US-0072885.
98US-0075026.
                                                                      87US-0021493
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                                                                                           87US-0021493
                                           HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                     58.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                  22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
0.005;
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 19
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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AAP82736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
To G1 is attached NH2 and to N22 is attached OH.
Magainins are a class of substantially pure, homogeneous
polypeptides composed exclusively of about 25 amino acids, having a
mol. wt. of about 2500 or less, being water soluble at a concentration
of greater than 5 mg/ml at neutral pH or in an aq. solution of
physiologic ionic strength. They are amphiphilic surface-seeking and ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing granted patent numbers. For further information please visit the Derw web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This magainin III polypeptide has a mol. wt. of 25kD or less, is water sol. and non-cytolytic to animal cells, incl. RECs, and is amphiphilic. It is an active antimicrobial agent being effective against both Gram-positive and -negative bacteria. It is also effective against fungi and protozoa. It is therefore useful as an antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                Magainin polypeptide; cytotoxic agent; antimicrobial agent; therapeutic; anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antimicrobial polypeptide cpds. positive and negative bacteria, fund
                                                                                                             -negative bacteria, fungi,
and spermicidal agents
                                                                                                                          New Magainin polypeptide(s) - active against Gram-positive and -negative bacteria, fungi, viruses and protozoa and as cytotox
                                                                                                                                                                                     Zasloff
                                                                                                                                                                                                                                      05-AUG-1987;
                                                                                                                                                                                                                                                   23-JUL-1987;
04-MAR-1987;
                                                                                                                                                                                                                                                                                                                                      USN7076734-N
                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP82736 standard; protein;
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See also AAP71206-07.
                                                                                       Disclosure;
                                                                                                                                                               WPI; 1988-105363/15.
                                                                                                                                                                                                                                                                                       23-JUL-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Magainin polypeptide
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10-DEC-1990
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                                                                                                                                                                                                              (USSH ) US
                                                                                                                                                                                                                                                                                                                                                                                     leukaemia;
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12; Conserv
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(first entry)
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                                                                                                                                                                                                                                     87US-0076734.
87US-0021493.
87US-0081793.
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                                                                                                                                                                                                                HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; 11pp;
                                                                                                                                                                                                                                                                                                                                                                                       HTLV III
                                                                                       English
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (III)
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fungi and
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                                                                                                                                                                                                                                                                                                                                                                                                 gent; spermicidal agent;
antitumour activity; contraceptive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0057;
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surface-seeking and have

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See also AAP82734-37.

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Analogues have the same activity as Megainin I and II coupled with insignificant haemolytic action against human red blood cells. Useful as antibiotics, fungicides, spermicides, in destroying tumors and as preservatives and in sterilisation of food etc.
                                                                                                                                                                                      Deletion analogues of Magainin I and II peptide(s) - having high activity against microorganisms with low haemolytic action against human red blood cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a broad spectrum of properties at physiologic ionic strength and pH. The polypeptide is a microbial agent capable of inhibiting the growth or proliferation of gram-positive and gram-negative bacteria, fungi, virus and protozoan species. They are also useful as therapeutic cytotoxic agents. This includes antitumour activity. They are useful as spermicides and as a contraceptive agent. Magainin is active against HTLV III in vitro and has the potential to reduce the infectivity of the AIDS virus indicating its use as a sterilant against the virus or as a chemotherapeutic agent for treating tree.
                                                                                                                                                                                                                                                                                                  (SCRI-) SCRIPPS CLINIC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Magainin II; antibiotic; spermicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analogue of Magainin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                               88US-0281981.
                                                                                                                                                                                                                                                                                                                                                          89WO-0005499.
         58.3%; 55
100.0%; Pr
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100.0%;
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              Score 63; DB; Pred. No. 0.0
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Pred. No.
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            DB 11; ; ; . 0.0057; ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor;
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                                      Length 22;
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Best Local
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                                                                            Magainin II; antibiotic;
                                                                                                      Deletion analogue of Magainin
                                                                                                                                  05-NOV-1990
                                                                                                                                                                                     AAR05734 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deletion analogues of Magainin I and II peptide(s) - having high activity against microorganisms with low haemolytic action against human red blood cells.
                                                                                                                                                            AAR05734;
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25;
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                                                               fungicide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1988;
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                                                               preservant.
                                                                                                                                                                                                                                                                                                                                                                  22 AA;
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                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotic; spermicide;
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                                                                                                                                                                                    protein;
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                                                                            spermicide;
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Pred. No.
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                                                                            cancer; tumor;
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and
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14-JUN-1990 WO9006129-A Synthetic.

fungicide;

preservant.

Deletion 05-NOV-1990 AAR05732 AAR05732 standard;

09-DEC-1988; 05-DEC-1989;

Matches Query Match Best Local (

Local

l Similarity 12; Conserv

Conservative

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22

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Claim 24;

Page 24;

28pp;

WPI; 1990-209623/27.

Cuervo

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Query Match Best Local Matches

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Best Local
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 Analogues have the same activity as Megainin I and II coupled with insignificant haemolytic action against human red blood cells. Useful as antibiotics, fungicides, spermicicdes, in destroying tumors and as preservatives and in sterilisation of food etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analogues have the same activity as Megainin I and II coupled with insignificant haemolytic action against human red blood cells. Uses as antibiotics, fungicides, spermicides, in destroying tumors and as preservatives and in sterilisation of food etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deletion analogues of Magainin I and II peptide(s) - having high activity against microorganisms with low action against human red blood cells.
                                                      Claim 23;
                                                                        Deletion analogues of Magainin I and II peptide(s) having high activity against microorganisms with leaction against human red blood cells.
                                                                                                                                        Cuervo JH,
                                                                                                                                                                                 09-DEC-1988;
                                                                                                                                                                                                     05-DEC-1989;
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                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                       fungicide;
                                                                                                                                                                                                                                                                                                  Magainin II;
                                                                                                                                                                                                                                                                                                                     Deletion analogue of Magainin II.
                                                                                                                                                                                                                                                                                                                                           05-NOV-1990
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                                                      Page
                                                                                                                                                                                                                                                                                       preservant.
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                                                                                                                                                                                                                                                                                                  antibiotic;
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                                                      24; 28pp; English
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100.0%;
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Pred. No.
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0.0057;
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RESULT 13
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Best Local S
Matches 12
                                      Query Match
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Matches 12
                                                                                                The substitution analogue has biological activity equal to or greater than the parent Magainin II peptide. The analogue is effective as antibiotic and can be used to inhibit, prevent or destroy the growth or proliferation of microbes such as Grampositive and Grampogative bacteria, fungi, viruses and protozoa. It can also be used as a spermicide to inhibit, prevent or destroy the motility of sperm and as anti-tumour agent to inhibit the growth of or destroy tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Magainin I; antibiotic;
                                                                                                                                                                                                     Claim 26; Page 55; 58pp; English.
                                                                                                                                                                                                                                  Substitution analogues of magainin I and II - having increased biological activity, useful as spermicide, antibiotic, antiviral
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                                                                               Sequence
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Modified-site
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                                      l Similarity
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GIGKFLHSAKKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiviral; antitumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analogue (XII).
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                                                                                AA;
                                                                                                                                                                                                                                                                                      Cuervo JH;
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Pred. No.
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RESULT 14

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RESULT 15
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                Magainin I; magainin II; substitution analogue; antibiotic; antiviral; antitumour.
                                                       Magainin
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See also AAR10639-47, AAR10657-63 and AAR10999.
                                                                            18-APR-1991
                                                                                                    AAR10642
                                                                                                                        AAR10642 standard;
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Substitution analogues of magainin I and II - having increased biological activity, useful as spermicide, antibiotic, antiviral and antitumour agents
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 26; Page 55; 58pp; English.
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antibiotic;
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                                                    II analogue (V).
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antiviral; antitumour.
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See also AAR10639-47, AAR10657-63 and AAR10999.
                                                                                                                                                                                                                                             Claim 26; Page 55; 58pp; English
                                                                                                Sequence
                                                                                                                                                                                                                                                                                  Substitution analogues of magainin I and II - biological activity, useful as spermicide, ant
                                                                                                                                                                                                                                                                         and antitumour agents
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               9 GIGKFLHSAKKF 20
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GIGKFLHSAKKF 12
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M;Contains: magainin 1; magainin 2
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Aug-2000
C;Accession: A28620; A29771
R;Terry, A.S.; Poulter, L.; Williams, D.H.; Nutkins, J.C.; Giovannini, M.G.; Moore, J. Biol. Chem. 263, 5745-5751, 1988
A;Title: The cDNA sequence coding for prepro-PGS (prepro-magainins) and aspects of ta;Reference number: A28620; MUID:88186892; PMID:2833514
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A28620
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38.0	38.4	38.4	38.4	38.4	38.4	38.9	38.9	38.9	38.9	38.9	38.9	38.9	38.9	38.9	38.9	
106	809	459	410	339	248	5105	600	544	380	337	337	325	205	204	190	
N	N	N	Н	N	N	ν	N	N	N	N	N	N	N	N	N	
T05199	T40537	F84935	S28615	в81258	F72262	T32650	T39516	S75388	T19096	S46254	A57011	A56406	C95351	D69097	A64039	
hypothetical prote	AAA family ATPase	argininosuccinate	serine/threonine/t	A/G-specific adeni	ubiquinone/menaqui	hypothetical prote	threonine ammonia-	probable phenylala	hypothetical prote	protein kinase CK1	casein kinase I-al	casein kinase I (E	VirB5 type IV secr	hypothetical prote	hypothetical prote	

## ALIGNMENTS

다 a Minimum DB Maximum DB

Scoring table: Sequence: Run on:

Database

RESULT 2 I40728 I40728 recombination protein recA - Corynebacterium glutamicum N;Alternate names: recombinase A C;Species: Corynebacterium glutamicum C;Date: 16-Aug-1996 *sequence revision 16-Aug-1996 *text_change 20-Apr-2001 C;Accession: I40728; S41939; I40727; S39258 R;Billman-Jacobe, H. DNA Seq. 4, 403-404, 1994 A;Title: Nucleotide sequence of a recA gene from Corynebacterium glutamicum. A;Reference number: I40728; MUID:95143581; PMID:7841463 A;Accession: I40728; MUID:95143581; PMID:7841463 A;Accession: I40728; MUID:95143581; PMID:7841463 A;Accession: I40728 A;Status: translated from GB/EMBL/DDBJ A;Cross-references: EMBL:X77384; NID:9475063; PIDN:CAA54563.1; PID:9475064 A;Experimental source: strain AS019	Query Match Best Local Similarity 100.0%; Pred. No. 0.012; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 9 GIGKFLHSAKKF 20	A;Accession: A28620 A;Molecule type: mRNA A;Residues: 1-303 <ter> A;Cross-references: GB:J03193; NID:g214654; PIDN:AAA49930.1; PID:g214655 R;Zasloff; M. Proc. Natl. Acad. Sci. U.S.A. 84, 5449-5453, 1987 A;Title: Magainins, a class of antimicrobial peptides from Xenopus skin: isolation, A;Reference number: A29771; MUID:87261003; PMID:3299384 A;Accession: A29771 A;Molecule type: mRNA A;Residues: 6-73,'Q',75-158,297-303 <zas> C;Superfamily: magainin precursor</zas></ter>
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R; Fitzpatrick, R.; O'Donohue, M.; JOy, J.; Heery, D.M.; Dunican, Appl. Microbiol. Biotechnol. 42, 575-580, 1994
A; Title: Construction and characterisation of recA strains of Cor A; Reference number: 140727; MUID:95134369; PMID:7765733
                                                                                                                                                                                                                     A; Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                               A; Reference number: A75001
A; Accession: C75035
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A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
                                                                                                                                                                                                                                                                                                                                                                                                                   R; anonymous, Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: plays an essential role in homologous recombination, C; Superfamily: recombination protein recA C; Keywords: ATP; DNA binding; DNA recombination; DNA repair; nucleot F; 78-85/Region: nucleotide-binding motif A (P-loop) F; 152-157/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 118-132,'I',134-169,'GN',172-190,'S',192-200 <FIT1>
A;Cross-references: EMBL:X75085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X75085; NID:g474416; PIDN:CAA52977.1; PID:g474417
R;Filzpatrick, R.; O'donohue, M.; Joy, J.; Heery, D.M.; Dunican, L.K.
submitted to the EMBL Data Library, September 1993
A;Description: Construction and characterisation of recA strains of Coryne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: I40727
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A; Residues: 1-102, 'DSF', 106-376 <BIL2>
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A; Reference number: S41939
A; Accession: S41939
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A; Residues: 118-200 <FIT2>
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                                                                                                                                                                                                                                                                                                           Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Pyrococcus abyssi
pate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
                                                                                      Matches
                                                                                                                                                                                                                                       Cross-references: GB:AJ248287; GB:AL096836;
                                                                                                                               Query Match
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9; Conserv
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KWKAYINLKQHGMGRVIREARKF 157
                                        KWKLF - - - KKIGIGKFLHSAKKF 20
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                                                                                      Conservative
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39.1%;
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                                                                               Pred. No. 3.5, 6; Mismatches
                                                                                                      Score 47.5;
Pred. No. 3
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Pred. No. 4.7;
4; Mismatches
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                                                                                                                          Length 237;
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                                                                                                                                                                                                                                       PIDN:CAB50176.1;
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RESULT 4

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C;Accession: T43022
R;Del Sorbo, G.; Andrade, A.C.; Van Nistelrooy J, G.M.; Van Mol. Gen. Genet. 254, 417-426, 1997
A;Title: Multidrug resistance in Aspergillus nidulans involv A;Reference number: Z07910; MUID:9180695; PMID:9180695
A;Accession: T43022
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T43022
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T50950
                                         A; Molecule type: DNA
A; Residues: 1-1562 <DEL>
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
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                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                                                                                  ATP-binding
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A; Introns: 30/3; 235/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.50
A;Experimental source: BAC clone B24P7; strain OR74A
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A; Residues: 1-491 <SCH>
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A; Residues: 1-427 <STO>
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A; Title: Complete genome sequence of the alkaliphilic bacterium
A; Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene:
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Cross-references: EMBL:Z68906; NID:e989397; PID:e219958; Experimental source: strain SAS56; clone bc-atra
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: T50950
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                                                                                                                                                                                                                                                                multidrug cassette transport
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Pred. No. 6
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Pred. No. 7
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                      PIDN:CAA93142.1
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A;Title: Identification and genetic analysis of normal and mutant phytoene synthase general A;Accession: S35154; MUID:93344508; PMID:8343597
A;Status: translation not the synthase synthase general and mutant phytoene synthase general and synthase general and synthase synthase general and synthase gener
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N;Alternate names: ripening protein 5

C;Species: Lycopersicon esculentum (tomato)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 02-Mar-2001
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 02-Mar-2001
C;Accession: S22474; S06321; S35155; S35154; S21981; S24967; S24968
R;Ray, J.; Moureau, P.; Bird, C.; Bird, A.; Grierson, D.; Maunders, M.; Truesdale, M.; E Plant Mol. Biol. 19, 401-404, 1992
A;Title: Cloning and characterization of a gene involved in phytoene synthesis from toma A;Reference number: S22474; MUID:92322971; PMID:1623189
A;Roccession: S22474
A;Molecule type: DNA
A;Residues: 1-412 <RAYY
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A;Introns: 188/3; 338/3; 655/3; 711/2; 814/1; 1356/3
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: Psyl
A;Introns: 138/1; 155/1; 212/3; 291/2; 355/3
C;Superfamily: Mycobacterium marinum phytoen
C;Keywords: chloroplast; transferase
                                                                                                              RESULT
A42102
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A;Title: Sequence of pTOM5, a ripening related cDNA from tomato.
A;Reference number: S06321; MUID:88096591; PMID:3697097
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A;Experimental source: mutant r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Crogs-references: EMBL:X67144;
A;Experimental source: mutant rY
A;Accession: S35154
A;Status: translation not shown
     phytoene synthase (EC 2.
C; Species: Lycopersicon
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A; Residues: 1-387, 'NMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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9; Conserv
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R:Lidholm, D.A.; Gudmundsson, G.H.;
FEBS Lett. 226, 8-12, 1987
A;Title: Insect immunity: cDNA clone
A;Reference number: S00208
A;Accession: S00208
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C;Date: 04-Mar-1993 *seq
C;Accession: A42102
R;Bartley, G.E.; Viitane
J. Biol. Chem. 267, 5036
A;Title: A tomato gene e
A;Reference number: A421
                                                                                     C;Species: Hyalophora cecropia (cecropia moth)
C;Date: 24-Sep-1981 #sequence_revision 04-Nov-1994 #text_change 18-Jun-1999
C;Accession: A40420; S00208; A91121; A93260; A01769
R;Gudmundsson, G.H.; Lidholm, D.A.; Asilng, B.; Gan, R.; Boman, H.G.
J. Biol. Chem. 266, 11510-11517, 1991
A;Title: The cecropin locus. Cloning and expression of a gene cluster encod. A, Reference number: A40420; MUID:91268009; PMID:1711035
A;Accession: A40420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Chambaud, I.; Heilig, N., 2001
R;Chambaud, I.; Heilig, N., 2001
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory
A;Title: The complete genome sequence of the murine respiratory
A;Title: The complete genome sequence of the murine respiratory
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A;Molecule type: DNA
A;Residues: 1-64 <GUDA
A;Residues: 1-64 <GUDA
A;Cross-references: GB-M63845; NID:g159196; PIDN:AAA29185.1; PID:g159197
A;Cross-references: GB-M63845; NID:g159196; PIDN:AAA29185.1; PID:g159197
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A; Residues: 1-412 <BAR>
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A;Genetic code: SGC3
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A;Experimental source: strain UAB CTIP
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A; Residues: 1-666 < KUR>
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9; Conserv
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A42102; MUID:92184738;
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1992
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Pred. No. 18;
5; Mismatches
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C; Keywords: oxidoreductase
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A;Residues: 1-925 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL54192.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nitrate reductase (EC 1.7.99.4) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: cecropin
C;Reywords: amidated carboxyl end; antibacterial; hemolymph
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-26/Domain: propeptide #status predicted <PRO>
F;23-26/Domain: propeptide #status experimental <PRO>
F;27-63/Product: cecropin A #status experi
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Proc. Natl. Acad. Sci. U.S.A. 80, 6475-6479, 1983
A;Title: Solid-phase synthesis of cecropin A and related peptides.
A;Reference number: A54966; MUID:84042494; PMID:6579533
A;Contents: annotation; chemical synthesis
A;Note: protein carboxyl-terminal composition and amidation determined by mass spectrome C;Comment: Cecropins are a family of basic peptides having lytic and antibacterial activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X06672; NID:g9413; PIDN:CAA29871.1; PID:g671870 R;Hultmark, D.; Engstrom, A.; Bennich, H.; Kapur, R.; Boman, H.G. Eur. J. Biochem. 127, 207-217, 1982 A;Title: Insect immunity: isolation and structure of cecropin D and four minor antibacte A;Reference number: A91121; MUID:83053366; PMID:7140755 A;Accession: A91121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
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A;Title: Sequence and specificity of two antibacterial proteins involved A;Reference number: A93260; MUID:81245158; PMID:7019715
A;Accession: A93260
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: BMEII0950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain 16M
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A;Accession: AE3628
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A;Rote: cecropin C lacks the carboxyl-terminal blocking
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A; Residues: 1-64 <LID>
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Pred. No.
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hypothetical protein SA1548 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May_2001 #sequence_revision 10-May_2001 #text_change 22-Oct-2001 C;Accession: C89957 T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L.; R;Kuroda, M.; Ohta, T; Kobayashi, N.; Sawano, T; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89957
A;Status: preliminary
A;Status: preliminary
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S65297
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C89957
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R;Duesterhoeft, A.; Floeth, M.; Fritz, M.; Hilbert, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Saccharomyces cerevisiae C; Date: 10-Dec-1994 #sequence_revision
                                                                                     F;224-240/Domain: transmembrane #status predicted <TM7>
                                                                                                             F;118-134/Domain: transmembrane #status predicted <TM4>F;143-159/Domain: transmembrane #status predicted <TM5>F;189-205/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z73620; NID:g1370544; PID:e246970; PID:g1370545; MIPS:YPL264
A;Experimental source: strain S288C (AB972)
                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-353 <DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Delius, H.; Hebling, U. submitted to the Protein
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A;Experimental source: strain S288C (AB972)
R;Delins H · UARITATION
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A; Residues: 1-205 < KUR>
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A;Residues: 1-353 <D
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                                                                                                                                                                                                ;16-32/Domain: transmembrane #status predicted ;54-70/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                 ;Keywords: transmembrane protein
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Search completed: June 6, 2003, 13:25:26 Job time: 14.5 secs
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C:Keywords: amidated carboxyl end; antibacterial
F:35/Modified site: amidated carboxyl end (Leu)
                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 1-35,'S' <QUX>
A; Note: the carboxyl end is blocked and was not sequenced directly
                                                                                                                                                                                                                                                                                                                                                                                                             Ev., X.; Steiner, H.; Engstrom, A.; Bennich, H.; Boman, H.G.
Eur. J. Biochem. 127, 219-224, 1982
A;Title: Insect immunity: isolation and structure of cecropins B and D from pupae of the A;Reference number: A91122; MUID:83053368; PMID:6754375
A;Accession: A01771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Craig, A.G.; Engstroem, A.; Bennich, H.; Kamensky, I. Biomed. Environ. Mass Spectrom. 14, 669-673, 1987
A;Title: Plasma desorption mass spectrometry coupled with conventional peptide sequencin A;Reference number: A54725; MUID:88108273; PMID:2962676
A;Accession: A54725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cecropin B - Chinese oak silkmoth
(;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Date: 17-Dec:1982 #sequence_revision 12-Apr-1996 #text_change 07-May-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable plcA protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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ARLY_BUCAL
BLA1_HAENI
KC1B_BOVIN
SYI_SCHAC
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9 antheraea p
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Pfam; PT00918; Gastrin; 1.

Cleavage on pair of basic residues; Repeat; Amphibian skin; Antibiotic; Fungicide; Hemolysis; Signal; 3D-structure.

18

POTENTIAL.
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PIR; A29771; A29771.
PDB; 2MAG; 08-APR-98.
InterPro; IPR001651; Gastrin.
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STRAIN-ATCC 13059 / AS019;
Varins S.M., Fitzpatrick R
                                                               Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteria (class); Actin
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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Fitzpatrick R., O'Donohue M., Joy J., Heery D.M., Dunican L.K.;

Fitzpatrick R., O'Donohue M., Joy J., Heery D.M., Dunican L.K.;

"Conynebacterium glutamicum and Brevibacterium lactofermentum.";

Appl. Microbiol. Biotechnol. 42:575-580(1994).

Appl. Microbiol. Biotechnol. 42:575-580(1994).

FIUNCTION. CAN CATALYZE THE HYDROXYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAS. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.

-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 01-AUG-1988
01-OCT-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 118-200 FROM N.A. STRAIN-ATCC 13059 / AS019; MEDLINE-95134369; PubMed-7765733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genomic sequence of Corynebacterium Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 13059
MEDLINE=95143581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases. \cite{MBL/GenBank/DDBJ}
                                                                                                                                                                                                                                                                  NP_BIND
CONFLICT
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Nakagawa S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of a recA gene from Corynebacterium DNA Seq. 4:403-404(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Billman-Jacobe H.;
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                                           PSY1_LYCES
P08196;
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EMBL; X75085; CAA52977.1; -.
HSSP; P26345; IG19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U14965; AAD12743.1; -. EMBL; X77384; CAA54563.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000229; RECA.
SMART; SMAA77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The European Bioinformatics Institutions as longues by non-profit institutions as longues.
                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00154; recA;
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001553; RecA.
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                                                                                                                                                                                                                                                                                            DNA damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                  334
                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                  KIFKKLGVGKY
                                                                                                                                                              KLFKKIGIGKF
                                                                                                                                                                                                                                                 376 AA;
                                                                                                                                                                                                                                                                                DNA recombination; 78 85 A
   (Rel. 08, Created)
(Rel. 30, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                             Conservative
                                                            STANDARD;
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PubMed=7841463;
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Pred. No.
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ATP (BY SIMILARITY).
A -> H (IN REF 2).
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EMBL; W84744; AAA34153.1; --
EMBL; Y00521; CAA68575.1; --
EMBL; X00441; CAA42969.1; --
EMBL; A21360; CAA01548.1; --
PIR; S0321; S06321.
PIR; S06321; S06321.
InterPro; IRB002060; Squ/phyt_
InterPro; IRB002060; Squ/phyt_
Pfam; PF00494; SQS_PSY; 1.

PROSITE; PS01044; SQUALEN_PHYTOEN_SYN_1; 1.

PROSITE; PS01045; SQUALEN_PHYTOEN_SYN_2; 1.

Multifunctional enzyme; Carotenoid biosynthesis;
Isoprene biosynthesis; Transferase; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesis from tomato.";
Plant Mol. Biol. 19:401-404(1992).
-I- FUNCTION: CATALYZES THE REACTION FROM PREPHYTOENE DIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-cv. Ailsa Craig;
MEDLINE-88095591; PubMed-3697097;
MEDLINE-88095591; PubMed-3697097;
Ray J., Bird C.R., Maunders M., Grierson
"Sequence of pTOM5, a ripening related of
Nucleic Acids Res. 15:10587-10587(1987).
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STRAIN-CV. Allsa Craig; TISSUE-Leaf;
MEDLINE-92322971; PubMed-1623189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Marmande;
MEDLINE=94071905; PubMed=8250898;
Roemer S., Hugueney P., Bouvier F.
"Expression of the genes encoding enzymes in Capsicum annuum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ray J., Moureau P., Bird C., Bird A., Grierson D., Maunders Truesdale M., Bramley P., Schuch W.; "Cloning and characterization of a gene involved in phytoen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bartley G.E., Viitanen P.V., Bacot K.O
"A tomato gene expressed during fruit
the carotenoid blosynthesis pathway.";
J. Biol. Chem. 267:5036-5039(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTER MEDLINE-92184738; PubMed-1544888;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Carotenoid biosynthesis.
SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Chloroplast.
DEVELOPMENTAL STAGE: IN SEEDLINGS
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CATALYTIC ACTIVITY: 2 ge
prephytoene diphosphate
CATALYTIC ACTIVITY: Prep
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SIMILARITY: BELONGS TO THE PHYTOENE/SQUALENE SYNTHETASE FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Res. Commun. 196:1414-1421(1993).
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protein pTOM5).
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he early carotenoid
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     Multigene family; Transit peptide.
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                                                                 Holak T.A., Engstroem A., Kraulis P.J., Lindeberg G., Bennich Jones T.A., Gronenborn A.M., Clore G.M., The solution conformation of the antibacterial peptide cecro nuclear magnetic resonance and dynamical simulated annealing Biochemistry 27:7620-7629(1988).
                        SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIAL
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: A PROTEIN WITH THE SAME SEQUENCE AS CECROPIN THE CARROXYI. BICCOURS.
                                                                                                                                                                                                         MEDLINE-81245188; PubMed-7019715;
Steiner H., Hultmark D., Engstroem A., Bennich H., Boman H.G.;
"Sequence and specificity of two antibacterial proteins involv
                                                                                                                                                                                                                                                                          Hultmark D., Engstroem A., Bennich H., Kar
"Insect immunity: isolation and structure
minor antibacterial components from Cecrop
Eur. J. Blochem. 127:207-217(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91268009; PubMed=1711035; Gan R., Boman H.G. Gudmundsson G.H., Lidholm D.-A., Aasling B., Gan R., Boman H.G. "The cecropin locus. Cloning and expression of a gene cluster encoding three antibacterial peptides in Hyalophora cecropia."; Biol. Chem. 266:11510-11517(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hyalophora cecropia (Cecropia moth).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Perrygota; Neoptera; Endopterygota; Lepidoptera; Olitrysia; Bombycoidea; Saturniidae; Saturniinae; Attacini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1988 (Rel. 07, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation Cecropin A precursor (Cecropin C).
                                                                                                                                               STRUCTURE BY NMR. MEDLINE=89088132; PubMed=3207693;
                                                                                                                                                                                                                                                                                                                                                                   cecropins A and FEBS Lett. 226:8
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                                                                                                                                                                                     Nature 292:246-248(1981).
                                                                                                                                                                                                                                                   PRELIMINARY SEQUENCE OF 27-63
                                                                                                                                                                                                                                                                                                                                                                  Lidholm D.-A., Gudmundsson G.H., Xanthopoulos K.G., "Insect immunity: cDNA clones coding for the precurs cecropins A and D. antibacterial proteins from Hyalo FEBS Lett. 226:8-12(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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          THE CARBOXYL BLOCKING GROUP, REF.3 AUTHORS.
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9; Conser
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45.0%;
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PHYTOENE SYNTHASE 1.
KLIALPIAYAKSLVPPTKT ->
QVDCITYCICKISCASYKN (IN REF.
KLIALPIAYAKSLVPPT ->
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Pred. No. 5
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Matches
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
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19-Dhospholipase C 1 precursor (EC 3.1.4.3) (MTP40 anticy)
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PIR; A40420; A40420.
PIR; S00208; S00208.
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InterPro; IPR003254; IIP_Cecropin.
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STRALNE-HJ/KV;
MEDLINE-98295987; PubMed-9634230;
MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
Cole S.T., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A species-specific nucleotide sequence of Mycobacterium tuberculosis encodes a protein that exhibits hemolytic activity when expressed in Escherichia coli.";
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                                                                                                                                                                                                                                     Johansen K.A., Gill R.E., Vasil M.L.; "Biochemical and molecular analysis of phospholipase phospholipase D activity in mycobacteria."; Infect. Immun. 64:3259-3266(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Infect. [2]
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M63845; AAA29185.1;
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L11868; AAB59164.1; ALT\_INIT L11868; AAB59165.1; ALT\_SEQ. U49511; AAC18943.1; -. Z83860; CAB06148.1; ALT\_INIT AE007081; AAK46709.1; -.

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Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Moliver S., Osborne J., Quail M.A., Rajandream M.A., Rog Rutter S., Seeger K., Skelton S., Squares S., Squares S., Islston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                       J. Clin. Microbiol. 35:1190-1195(1997).

-i- FUNCTION: HYDROLYZES SPHINGOWYELIN IN ADDITION
-i- FUNCTION: HYDROLYZES SPHINGOWYELIN IN ADDITION
-i- FUNCTION FOR THE PROBABLE VIRULENCE FACTOR
PATHOGENESIS OF M. TUBERCULOSIS AT THE LEVEL OF
SURVIVAL, BY THE ALTERATION OF CELL SIGNALING E
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Parra C.A., Londono L.E., del Portillo P.
"Isolation, characterization, and molecul
Mycobacterium tuberculosis antigen gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White C Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White C Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Miku
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Analysis of genetic polymorphism Mycobacterium tuberculosis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specific sequence.";
rnfect. Immun. 59:3411-3417(1991).
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"Analysis of gen
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CAUTION: REF.5 AND REF.6 SEQUENCE DIFFERS FROM THAT S
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sen the Swiss Institute of Bioinformatics and the En
Suropean Bioinformatics Institute. There are no rest
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phospholipase
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                                                                                                                InterPro; IPRUUJZZZ,
Pfam; PF00272; cecropin; 1.
Pronom; PD003996; IIP_cecropin; 1.
PROSITE; PS00266; CECROPIN; 1.
PROSITE; PS00266; CECROPIN; 1.
Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.
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AMIDATION.

7 APRESE 35; AMIDATION.
                                                                                                                                                                                                                                                                                                 MEDLINE-88108273; PubMed-2962676;
Craig A.G., Engstrom A., Bennich H., Kamensky I.;
"Plasma desorption mass spectrometry coupled with conventional peptide sequencing techniques.";
Blomed. Environ. Mass Spectrom. 14:669-673(1987).
-i- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
-I- SUBCELLULAR LOCATION: Secreted.
-I- SUMILARITY: BELONGS TO THE CECROPIN FAMILY.
PIR; A01771; CKAOBP.
PIR; A54725; A54725.
InterPro; IPR000875; Cecropin.
InterPro; IPR000875; Cecropin.
InterPro; IPR000875; Cecropin.
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MEDLIND-83053368; PubMed-6754375;

QU X.-M., Steiner H., Engstroem A., Bennich H., Boman H.

"Insect immunity: isolation and structure of cecropins E
pupae of the Chinese oak silk moth, Antheraea pernyi.";

Eur. J. Biochem. 127:219-224(1982).
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EMBL; S69737;
TIGR; MT2416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antheraea pernyl (Chinese oak silk moth).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Eukaryota; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Saturniidae; Saturniinae; Saturniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-APR-1990 (Rel. 14, Last sequence u)
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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S69737; AAC60465.2;
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BINDING
ACT_SITE
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                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Probable mannitol dehydrogenase 3 (EC 1.1.1
mannitol dehydrogenase 3).
                     Stylosanthes humilis (Townsviile stylo).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae;
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Q43138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z35637; CAA84685.1; -HSSP; Q06486; 1CKI.
WormPep; C03C10.1; CE00872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CASEIN KINASE I SUBFAMILY.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative casein kinase I C03C10.1 in chromosome
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InterPro; IPR002290; Ser_thr_pkinase.
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PROTEIN_KINASE_ST; 1.
PROTEIN_KINASE_DOM; 1.
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Matches 7
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Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OXIDIZES MANNITOL TO MANNOSE. PROVIDES THE INITIAL STEP
BY WHICH TRANSLOCATED MANNITOL IS COMMITTED TO CENTRAL METABOLISM
AND, BY REGULATING MANNITOL POOL SIZE, IS IMPORTANT IN REGULATING
SALT TOLERANCE AT THE CELLULAR LEVEL (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: D-mannitol + NAD(+) = D-mannose + NADH.
-!- COPACTOR: ZINC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                    VNUC_INCCA
P08028;
01-AUG-1988
01-AUG-1988
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended the European Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-cv. Paterson;
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METAL
                       This
                                                               MEDLINE=85170522; PubMed=6532006;
Nakada S., Creager R.S., Krystal M., Pal
"Complete nucleotide sequence of the inf
nucleoprotein gene.";
Virus Res. 1:433-441(1984).
-!- FUNCTION: ENCAPSIDATES THE NEGATIVE
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InterPro; IPR002085; Adh_zn_family.
Pfam; PF00107; adh_zinc; 1.
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                                                                                                                                                                                                                                                                       Viruses; ssRNA negative-strand Influenzavirus C.
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                       SWISS-PROT
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an email to license@isb-sib.ch).
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entry is copyright. It is produced through a ciss Institute of Bioinformatics and the EMBL
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Last annotation updat
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (SECOND ATOM) (BY SIMILARITY).
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                                                                                                                                         C/California/78
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Pfam; PR00037; fer4; 3.
Pfam; PF01077; NIR\_SIR\_ferr;
Pfam; PR03460; NIR\_SIR\_ferr;
PRINTS; PR00397; SIROHAEM.

PS00198;

4FE4S\_FERREDOXIN;

InterPro; IPR000660; InterPro; IPR005117;

Nir\_sir\_fer 4Fe4S\_ferredoxin EMBL; U67531; HSSP; Q45560;

AAB98876.1; 1BWE.

TIGR; MJ0870;

InterPro; IPR001450;

entities requires a license agreement (or send an email to license@isb-sib.ch)

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01-NOV-1997
16-OCT-2001
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MEDLINE-96337999; pubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaihe B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus

jannaschii.";
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-i- SIMILARITY: TO COENZYME F420 HYDROGENASE BETA SUBUNIT.
-i- SIMILARITY: TO M.JANNASCHII MJ1349, MJ0725 AND MJ0551.
-i- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
-i- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
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RT "The genome sequence of Schizosaccharomyces pombe.";
RT "The genome converts alpha-aldose to the beta-anomer. It is active on D-clucase. L-arabinose. D-volcase. D-volcase. D-volcase.
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Hypothetical protesic
Complete proteome.
METAL 428
METAL 434
METAL 468
METAL 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAL10 bifunctional protein [Includes: UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase); Aldose 1-epimerase (EC 5.1.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAL10 OR SPBPB2B2.12C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALX_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        оэнриз;
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                                                 is active on D-glucose, L-arabinose, D-xylose, maltose and lactose (By similarity).

CATALYTIC ACTIVITY: UDP-glucose = UDP-galactose CATALYTIC ACTIVITY: Alpha-D-glucose = beta-D-glucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gwilliam R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620
                          Galactose metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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468
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metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY
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                                                                        UDP-galactose.
se = beta-D-glucose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyne M., Lyne R., Stewart
                       step
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CECB_HYACE
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ACT_SITE
SEQUENCE
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EPIMERASE FAMILY.
-!- SIMILARITY: IN THE
EPIMERASE FAMILY.
                 Boman H.G., Faye I., Xanthopoulos K.G., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hyalophora cecropia (Cecropia moth).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; G
Ditrysia; Bombycoidea; Saturniidae; Saturniinae; Attacini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CECB_HYACE
P01508;
Xanthopoulos
Andreu D.;
                                                                                                                              Proc.
                                                                                                                                                                                van Hofsten P., Faye I.
Roman I.A., Boman H.G.,
                                                                                                                                                                                                                                                                                      "The structure of the gene for cecropin protein from Hyalophora cecropia."; Eur. J. Biochem. 172:371-376(1988).
                                                                               SEQUENCE
                                                                                                                  "Molecular cloning, cDNA sequencing, and chemical cecropin B from Hyalophora cecropia."; Proc. Natl. Acad. Sci. U.S.A. 82:2240-2243(1985).
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-88166708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cecropin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel.
13-AUG-1987 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01370; Epimerase; 1.
TIGRFAMS; TIGR01179; galE; 1.
PROSITE; PS00545; ALDOSE_1_EPIMERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001823; Ald1_epimerase.
InterPro; IPR001509; Epimerase_Dh.
InterPro; IPR001205; NAD_binding.
Pfam; PF01263; Aldose_epim; 1.
Pfam; PF01370; Epimerase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                         MEDLINE-86005745;
                                                                                                                                                                                                                               MEDLINE=85190472;
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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P09147; 1XEL.
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9; Conser
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350
713
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                                                         PubMed=3840100;
                                                                                                                                                                                                  PubMed=3857578;
aye I., Kockum K.,
                                                                                                                                                                                                                                                                                                                                                                            PubMed=3127206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01, Created)
05, Last sequence up
41, Last annotation
               Bennich H., Engstr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 N
80666 MW;
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47.4%;
                                                                                                                                                                          Engstroem A., Andreu D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isomerase;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAROTASE (POTENTIAL).
51C89DA0843A8556 CRC64;
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             Engstroem A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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No. 32;
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                                                                                                                                                                                                                                                                                                                                                        Kockum
             Kockum K., Lee J.-Y.,
roem A., Merrifield R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                  Β,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                  , Faye I., Boman antibacterial in
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                                                                                                                                                                                Xanthopoulos ., Merrifield
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                                                                                                                                                               유. <sup>교</sup> 조
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RESULT 13
CECA_BOMMO
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Best Local S
Matches 7
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EMBL; X07404; CAA30306.1; ...
EMBL; M3924; AAA29187.1; -..
PIR; A01770; CKWKB.
PIR; S02606; S02606.
InterPro; IPR000875; Cecropin.
InterPro; IPR003254; IIP_cecropin.
Pfam; PF00272; Cecropin; 1.
ProDom; PD003996; IIP_cecropin; 1.
PROSITE; PS00268; CECROPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
SIGNAL
                                                                                                                                                                                                                              Q27239;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "On the pri
Hyalophora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insect immunity.";
Nature 292:246-248(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 27-61.
MEDLINE=81245158; PubMed=7019715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steiner H., Hultmark D., Engstroem A., Bennich H., Boman 
"Sequence and specificity of two antibacterial proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steiner H.,
                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Ditrysia; Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
Yamano Y., Matsumoto M., Inoue K., Kawabata T., Morishin "Cloning of cDNAs for cecropins A and B, and expression in the silkworm, Bombyx mori.",
Biosci. Biotechnol. Biochem. 58:1476-1478(1994).
                                                                                                                                                                                                      Cecropin A precursor.
                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                  STRAIN=C1
                                                                                                                                                                           Bombyx mori (Silk moth)
                                                                                                                                                                                                                                                                      CECA_BOMMO
                                                                   MEDLINE=94369101; PubMed=7765280;
                                                                                              SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=7091;
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immunity; Antibiotic; Hemolymph; Amidation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 42;
Pred. No.
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65E309CB2983BD61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CECROPIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REMOVED BY A DIPEPTIDYLPEPTIDASE
                                                                                                                                                                                                                                                                        PRT;
                                                                                 body;
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     AND ANTIBACTERIAL ACTIVITY AGAINST
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Lepidoptera; (
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proteins involved
                                  , Morishima 1.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDE
                                                                                                                                                     ; Hexapoda;
Glossata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROUP).
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN FAT BODY AND HEMOCYTES.
-!- SIALSO EXPRESSED IN MALPIGHIAN TUBE AND TO A MUCH LESSER EXTENT IN MIDGUT. NOT PRESENT IN SILK GLAND.
-!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D17394; BAA04217.1; ...
EMBL; S74376; AAC60515.1; ...
InterPro; IPR000875; Cecropin.
InterPro; IPR003254; IIP_cecropin.
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P44279;
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CHAIN
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                                                                                                                MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Mite O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weidman J.F., Phillips C.A., Spriggs T., Baudek D.M., Brandon R.C., Pine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfam; pF00272; cecropin; 1.
proDom; pD003996; IIP_cecropin; 1.
proSITE; pS00268; CECROPIN; 1.
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
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                                                          Science
                                                                                                     Venter J.C.
                                                                                      Whole-genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                 (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat)
1 protein HI1631 precursor.
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                                                                                       sequencing
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                                                                                                                                                                                                                                                                                                                          gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CECROPIN A.
AMIDATION (G-62 |
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB Pred. No. 4.1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
BY SIMILAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6A1C39975516D86A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
                                                                                       and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                              190
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                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 15

KC1A_BOVIN

ID KC1A_BOVIN

ID KC1A_BOVIN

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Best Local
                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr modified and this statement is not removed. Usage by and or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          "Ovine casein kinase I alpha gene.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS
EMBL; M76543; AAA30451.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-Rabbit; TISSUE-Skeletal muscle;
Zhai L., Depaoli-Roach A.A., Roach P.J.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
SPECLES-BOVINE; TISSUE-Brain;
MEDLINE-92052129; PubMed-1946367;
ROWLES J., Slaughter C., Moomaw C., Hsu J., Cobb M.H.;
"Purification of casein kinase I and isolation of cDNAs encoding multiple casein kinase I-like enzymes.";
Proc. Natl. Acad. Sci. U.S.A. 88:9548-9552(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine),
Oryctolagus cuniculus (Rabbit), and
Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartlodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KC1A_BOVIN
P35506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-Sheep; TISSUE-Blood; Yamamoto N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-1902 (Rel. 41, Last annotation update)
Casein kinase I, alpha isoform (EC 2.7.1.-) (CKI-alpha) (CKI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
NCBI_TaxID=9913, 9986,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Signal; Complete proteome.

SIGNAL 1 28 POTENTIAL.

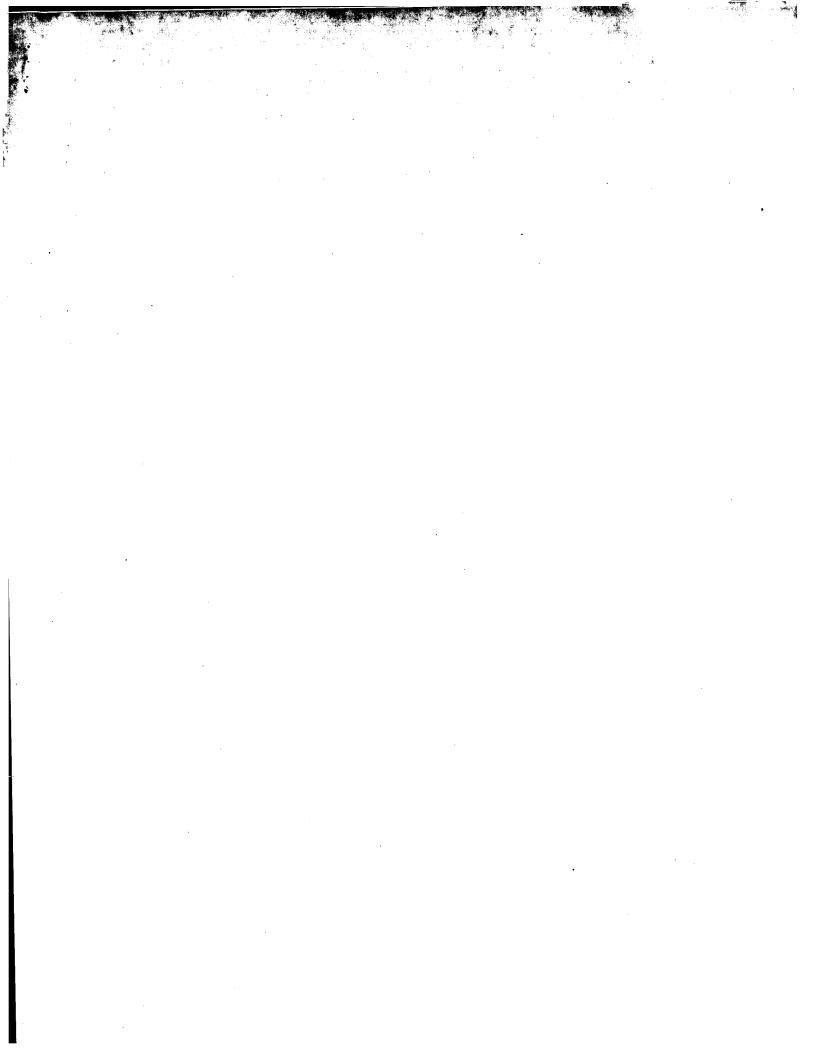
CHAIN 29 190 HYPOTHETICAL PROTEIN HI1631.

SEQUENCE 190 AA; 22314 MW; E4E3A8C7957EC908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                         SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CASSIN KINASE I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.9%;
36.8%;
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Pred. No. 11;
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                                                               (See http://www.isb-sib.ch/announce/
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                                                                                                                There are no restrictions ng as its content is in
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DOMAIN 17
NP_BIND 23
BINDING 46
ACT_SITE 136
SEQUENCE 325 AA;
                                                                                                                                                        Prodom; PD000001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                   InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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  16
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                     μ
                                        Similarity 61.8
8; Conservative
KYKLVRKIGSGSF
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                                                                                                                                           0011; PROTEIN_KINASE_DOM; 1.
Serine/threonine-protein kinase; ATP-binding;
                                                                                285 P
31 A
46 A
136 B
136 B
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                                                 Score 42; DB
Pred. No. 19;
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ATP (BY SIMILARITY).
BY SIMILARITY.
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Search completed: June 6, 2003, 13:23:58 Job time: 8 secs



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Result
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   protein search, using sw model
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175.359 Million cell updates/sec
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Q9UZ83
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Q9KU53
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ogk5p7 bacillus ha
Og6u53 neurospora
O60034 botrytis ci
O8vye2 arabidopsis
O40166 lycopersico
O98qc7 mycoplasma
O9ain5 carsonella
O9cy15 mus musculu
O9u2n8 caenorhabdi
O8ybf0 brucella me
O9td7 staphylococ
O08980 saccharomyc
O9vn08 drosophila
                                                                                                                                                          Description
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Q9uz83 pyrococcus
Q9k5p7 bacillus ha
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Q8QZG8	Q8QZG9	Q8QZH0	Q8QZH1	Q8QZH2	Q8QZH3	Q8QZH4	Q8QZH5	Q8QZH6	Q8QZH7	Q8QZH8	Q8QZH9	QBQZIO	Q8QZ11	292117	Q9Q1 <b>Y</b> 9	Q9Q1Z1	Q9Q1Z3	Q9Q1Z5	Q9Q127	Q9Q1Z9	Q9Q201	Q9Q203	Q9Q205	Q9Q2P4	Q9Q217	Q9IQ50	Q9IQ51	
8qz	8g2	892	Q8qz1	8gz	8	æ	8	8	8	8	æ	8	8	9	9	9.	8	9	9	8	9	9	8	9	۶	9	9	1
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## ALIGNMENTS

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RESULT 2
Q9UZ83
ID Q9UZ83
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Q8RC36

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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-MB4T / JCM11007;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., M
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
EMBL; AE013330; AAM23882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 309 AA; 34754 MW;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
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9; Conserv
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PRELIMINARY;
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PRT;
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Ma Y., Ling
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01-OCT-2000
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01-MAR-2002
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Arginase related (EC 3.5.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Pyrococcus abyssi genome sequence: insights into structure and evolution.", submitted (JUL-1999) to the EMBL/GenBank/DDBJ data EMBL, AJ248287; CAB50176.1; -. InterPro; IPR000287; Arginase. Pfam; pF00491; arginase; 1. PROSITE; PS00148; ARGINASE_2; UNKNOWN_1.
                                                                                                                                                                                          Pfam; PF02371; Transposase_20; 1. Pfam; PF01548; Transposase_9; 1.
                                                                                                                                                                                                                                                                        "Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison wit Nucleic Acids Res. 28:4317-4331(2000).

EMBL; APO01520; BAB07760.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9K5P7
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InterPro; IPR002525; Transposase_9.
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Fuji F., Hirama C., Nakamura Y., O
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
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Archaea; Euryarchaeota;
                                                                                                                                                         SEQUENCE
                                                                                                                                                                           Hypothetical
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427 AA; 49
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                                                                                           Score 47.5;
Pred. No. 18;
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Pred. No. 9.9;
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Ogasawara N.,
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Schulte U., Aign V.,
Nyakatura G., Mewes F
Submitted (JUL-2000)
                                                                                                                                                                                                                                                                                                            01-AUG-1998
01-AUG-1998
01-JUN-2002
                                                     Mol. Gen. Genec. ____ TO -!- SIMILARITY: BELONGS TO CAA93142.1;
                                                                                                                                                                                                                                                      ATP-binding multidrug cassette transporter. Botrytis cinerea (Botryotinia fuckeliana). Eukaryota; Fungi; Ascomycota; Pezizomycotina; Helotiales; Sclerotiniaceae; Botryotinia. NCBI_TaxID=40559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000822; Znf_C2H2.

SMART; SM00355; ZnF_C2H2; 3.

PROSSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_2.

DNA-binding; Hypothetical protein; Zinc-finger.

SEQUENCE 501 AA; 56866 MW; 5B7D09A2ED6C90E9
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                   EMBL; Z68906; CAA93142.1; --
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transpc
InterPro; IPR000577; FGGY_kin.
                                                                        binding cassette transporters.";
Mol. Gen. Genet. 254:417-426(1997)
                                                                                                                                                                                                                                                                                                                                            060034;
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Submitted (NOV-2001) to the
EMBL; AL389890; CAD11797.1;
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Eukaryota; Fungi; Ascomycota; Pezizom;
Sordariales; Sordariaceae; Neurospora
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01-DEC-2001 (TrEMBLrel. 19, Last
01-DEC-2002 (TrEMBLrel. 21, Last
01-JUN-2002 (TrEMBLrel. 21, Last
Hypothetical 56.9 kDa protein.
InterPro; IPRO
Pfam; PF00005;
                                                                                               De Waard M.;
"Multidrug resistance
                                                                                                                       De1
                                                                                                                                                                            in the plant pathogenic submitted (APR-2000) to
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                                                                                                                                             STRAIN-SAS56;
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Characterization
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           IPR001092;
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of a P-glycoprotein-like multi
ogenic fungus Botrytis cinerea.
00) to the EMBL/GenBank/DDBJ da
                                                                                                                    PubMed=9180695;
Nistelrooy H.,
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H.W., Mannhaupt G.;
to the EMBL/GenBank/DDBJ
                    ABC_transportr FGGY_kin.
           HLH_basic
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Pred. No. 21;
4; Mismatches
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the Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Yu G., Bowser L.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
A Carninci P., Chen M., Warusaka M., Nguyen M., Palm C.J.,
A Sakurai T., Satcu M., Seki M., Shinn P., Southwick A., Shinozaki K.,
Telli Length CDNA of gene At1g55900 (GI:15222797).";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Therero: IPRO04274, NIF.
NR Interpro: IPRO04274, NIF.
NR Pfam; PF03031; NIF; 1.
WHOLDERCE 376 AA; 42639 MW; 160466DD597215AA CRC64;
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12 6 kDa pro
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09LG22;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
E14J16.15;
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Best Local (
                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE FROM N.A.
                                                                                                                                         Arabidopsis thaliana (Mouse-ear
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
PROSITE; PS002445; FGGY_KINASES_2; UNKNOWN_1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
ATP-binding; Transport.
SEQUENCE 1562 AA; 173535 MW; 89036ECCE3D24919 CRC64;
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7; Mismatches
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STRAIN-AILSA CRAIG; TISSUE-PERICARP;
MEDLINE-93344508; PubMed-8343597;
                                                                                                                            Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                               GTOM5
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EMBL; AC002304; AAF79316.1; -.
InterPro; IPR004274; NIF.
Pfam; PF03031; NIF; 1.
SEQUENCE 414 AA; 46605 MW; ID21A52D01F8D413 CRC64;
                                                                                                                         NCBI_TaxID=4081;
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InterPro; IPR002060; Squ/phyt_synthse.
InterPro; IPR002049; SQS_PSY; 1.
PROSITE; PS01044; SQS_PSY; 1.
PROSITE; PS01045; SQUALEN_PHYTOEN_SYN_2; 1.
SEQUENCE 432 AA; 48775 MW; F609DOCF3272317D CRC64;
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Chambaud I., Heilig R., Ferris S., B.
Moszer I., Dybvig K., Wroblewski H.,
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01-JUN-2001 (TrEMBLrel.
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Ribosomal protein S19.
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Nucleic Acids Res. 29:2145-2153(2001).
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SEQUENCE 666 AA; 79222 MW; D69F28C79661E378 CRC64;
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MypuList; MYPU_4390;
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Clark M.A., Baumann L., Thao M.L., Mora "Degenerative Minimalism in the Genome J. Bacteriol. 183:1853-1861(2001). EMBL; AF250389; ARX18640.1; -- HSSP; P80381; 1QKF.
                                                                                                                                                                                                                                                                                                               Carsonella ruddii
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XA Arakawa T., Hara A., Fukunishi Y., Konno H., Kadchi J., Fukuda S.,
XA Arakawa T., Hara A., Fukunishi Y., Konno H., Kadchi J., Fukuda S.,
XA Arakawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
XA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
XA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Salto R.,
XA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Salto R.,
XA Aizawa K., Izawa M., Ashburner M., Batalov S., Yamanaka I.,
XA Aizawa K., Izawa M., Ashburner M., Batalov S., Yamana H.,
XA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Coasavant T.,
XA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Quackenbush J.,
XA Kadota K., Matsuda H.A., Nashior T., Pesole G., Quackenbush J.,
XA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
XA Kuchi P., Lewis S., Matsuo Y., Nashio T.,
XA Kuchi P., Lewis S., Matsuo N., Carninci P., de Bonaldo M.F.,
XA Schriml L.M., Staubli F., Solunga N., Carninci P., de Bonaldo M.F.,
XA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
XA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
XA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
XA Blake J., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
XA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
XA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
XA Nordone P., Ring B., Kaniya M., Lee N.H.,
XA Nordone P., Storch K., Schoenbach C., Seya T., Shibata Y., Storch K., F.,
XA Sasaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
XA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                       Query Match
Best Local
                                                                                                                                                           Nature 409:685-690(2001).

EMBL; AK017557; BAB30803.1; -.

HSSP; P04284; 1CFE.

MGD; MG1:191770; 5730414A08Rik.

InterPro; IPR001283; Allrgn_V5/Tpx1.

Pfam; PF00188; SCP; 1.

PRINTS; PR00837; V5TPXLIKE.

PTODOM; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002222; Ribosomal_S19.
pfam; pF00203; Ribosomal_S19; 1.
pRINTS; pR00975; RIBOSOMALS19.
proDom; pD001012; Ribosomal_S19; 1.
TIGRFAMS; TIGR01050; rpsS_bact; 1.
PROSITE; PS00323; RIBOSOMAL_S19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9CYL5;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5730414A08RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5730414A08Rik protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                   Wynshaw-Boris A., Yoshida K.,
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      Hayashizaki
                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
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   109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KMIGLNIFVHNGKKF
                                                                       Similarity
8; Conserv
   WKNTKKIGVGK
                                 WKLFKKIGIGK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                   154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.7%;
                                                                                                                                                   17090 MW;
                                                                                             41.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17,
17,
21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                           Score 45; DB:
Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 9.3;
Nismatches
                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153ABE6203FB60D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _S19
                                                                                                                                                     0F00D6180D0B5FFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                                                                            CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 88;
                                                                               2;
                                                                                                                  Length 154;
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                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                            collection.";
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; Murinae; Mus
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Q8YBF0
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Best Local S
Matches 7
                                                   InterPro; IPRUU1*0,, Pfam; PF00384; molybdopterin; 1. Pfam; PF01568; Molydop_binding; 1. Pfam; PF01568; MOLYBDOPTERIN_PF
   Oxidoreductase; SEQUENCE 925
                                                                                                                                                                              Brucella melitensis.
Bacteria, Proteobacteria,
                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                        Q8YBF0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000
01-MAY-2000
01-OCT-2001
                                                                                                                                                                        Brucellaceae; Brucella
                                                                                                                                                                                                 BMEII0950.
                                                                                                                                                                                                      Nitrate reductase
                                                                                                                                                                 NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01827; DUF38; 1. Pfam; PF00646; F-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y37H2A.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y37H2A.8 protein.
                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     Science 282:2012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9U2N8;
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                                                                                                                                                                                                                                                                                                                                                                                                             nvestigat
                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                       249
                                                                                                                                                                                                                                                                                                     ب
               PS00490; MOLYBDOPTERIN_PROK_2; PS00932; MOLYBDOPTERIN_PROK_3;
                                                                                                                                                                                                                                                                                                                     Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                    KWKLFKKIGIGKFLH 15
                                                                                                                                                                                                                                                                                     EWKMSKDTKLGKFFH 263
                                                                                                                                                                                                                                                                                                                                                                           32863; CAB60572.1;
IPR002900; DUF38.
IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                    319 AA;
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                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                           biology
Complete protectAA; 102574 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   2018(1998).
                                                                                                                                                                                                       alpha
                                                                                                                                                                                                                                                                                                                                                   37863 MW;
                                                                                                                                                                                                                                                                                                                           41.78;
46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematoda;
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                                                                                                                                                                                                     20, Cr
20, La
21, La
chain
          proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13,
13,
18,
                                                                                                                                                                           alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oda; Chromadorea; Caenorhabditis.
                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
in (EC 1.7.99.4).
                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                  Score 45; DB
Pred. No. 35;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                              PRT;
15278350CB06033F CRC64;
                                                                                                                                                                                                                                                                                                                                                 69C3C1E2CEA8FD14 CRC64;
                                                                                                                                                                                                                                             925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319
                                                                                                                                                                                                                                                                                                                         DB
35;
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                                                                                                                                                                                                                                                                                                                   <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases
                                                                                                                                                                                                                                                                                                                                  Length 319;
                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                 Gaps
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Q08980 ID Q08980 ID Q08980 AC Q08980 DT Q1-NO DT Q1-VQ QDT Q1-VQ QDT Chrom GN YPL26 OS Sacch OC Sacch OC Sacch OC NCBI [1] RP SEQUE RA Deliu RL Submi
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Q99TD7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                 Q08980 PRELIMINARY;
Q08980;
Q1-NOV-1996 (TrEMBLrel. 01, C2
01-NOV-1996 (TrEMBLrel. 01, L2
01-JUN-2002 (TrEMBLrel. 21, L2
Chromosome XVI reading frame (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
  SEQUENCE FROM N.A.
Delius H., Hebling U
Submitted (JUN-1996)
                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                              Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                         Eukaryota;
                                                                                                                                                                                        YPL264C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP003363; BAB57889_1; --
EMBL; AP003134; BAB42816.1; --
EMBL; AP003134; BAB42816.1; --
InterPro; IPR002123; Acyltransferase.
InterPro; IPR004552; AGP_acyltrn.
Pfam; PF01553; Acyltransferase; 1.
TIGRRAMS; TIGR00530; AGP_acyltrn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEQUENCE 205 AA; 23074 MW; 0078A4DCE66D218E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome sequencing of meticillin-resistant aureus.";
Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., I
Cui I., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., I
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R. I
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzak
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yosh
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315). Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical protein SAV1727.
SAV1727 OR SA1548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99TD7;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21311952; PubMed=11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus.
NCBI_TaxID=158878,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q99TD7
                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 55.0
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
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                                                                                                                                         Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                      Ascomycota;
                              ۵.;
                                                                                                                 Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158879;
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    the
                                                                                                                                                                                                        Last
Last
e ORF
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.
                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ب</u>
                                                                                                                                  Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                            Saccharomyces
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K., Yoshino C., S
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Page 6
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RN [2]
RP SEQUENCE FROM N.A.
RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
RI SUBMITTED (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE 353 AA; 39702 MW; 68A971BC5DB92988 CRC64;
DR FIRM; PFO0892; DUF6.
DR FIRM; PFO0892; DUF6.
DR SEQUENCE 353 AA; 39702 MW; 68A971BC5DB92988 CRC64;
DR FIRM; PFO0892; DUF6.
DR SEQUENCE 353 AA; 39702 MW; 68A971BC5DB92988 CRC64;
DR SEQUENCE 354 AA; 39702 MW; 68A971BC5DB92988 CRC64;
DR SEQUENC
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Result
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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         protein search, using sw model
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Match
       BLOSUM62
Gapop 10.0 , Gapext 0.5
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133.213 Million cell updates/sec
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108
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Copyright (c) 1993 - 2003 Compugen Ltd.
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- cspn__K/ptodata/2/pubpaa/pcr_NEW_PUB.pep: *
- cspn__K/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
- (cspn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
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/cgn2_6/ptodata/2/pubbaa/US08_PUBCOMB.pep:*
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US-09-908-139-6
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US-09-904-753-131
US-09-908-139-121
US-09-908-139-9
US-09-908-139-3
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Sequence 146, Appli
Sequence 17, Appli
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Sequence 3, Appli
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Sequence
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## ALIGNMENTS

RESULT 1 US-10-081-418-1

Sequence 1, Application US/10081418, Publication No. US20030096745A1 GENERAL INFORMATION:

APPLICANT: HAIM, Kyung-Soo
APPLICANT: LEE, Dong Gun
APPLICANT: LEE, Dong Gun
APPLICANT: LEE, Dong Gun
APPLICANT: LEE, Dong Gun
APPLICANT: KIM, Hee Nam
TITLE OF INVENTION: NO. US20030096745Alel peptides with increased + charge.
TITLE OF INVENTION: substituting one or more amino acids of CA-MA peptide
TITLE OF INVENTION: pharmaceutical compositions containing thereof
FILE REFERENCE: 428.1014

and hyd and

CURRENT APPLICATION NUMBER: US/10/081,418
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Kopatentin 1.71
SEQ ID NO 1
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

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; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-908-139-6
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                                                                                                                                                                                                RESULT 4
US-09-904-753-2
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APPLICANT: Owen, Donald R.
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELX027
CURRENT PELLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
Sequence 2, Application US/09904753

Publication No. US20030092612A1

GENERAL INFORMATION:
APPLICANT: LYJOOS, Robert T
TITLE OF INVENTION: Use of Antimicrobal Peptides as Preservatives in
TITLE OF INVENTION: Ophthalmic Preparations, Including Solutions,
TITLE OF INVENTION: Emulsions, and Suspentions
FILE REFERENCE: 2973 ver 2
CURRENT APPLICATION NUMBER: US/09/904,753
CURRENT FILING DATE: 2001-07-13
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LENGTH: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR FILE REFERENCE: 07422/016001
CURRENT APPLICATION NUMBER: US/09/908,139
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION UNMBER: 09/143,124
PRIOR APPLICATION UNMBER: 09/143,124
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
NUMBER: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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Similarity 72.2%;
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Woods, Donald
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pred. No. 0.0017;
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Pred. No.
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RESULT 6
US-09-04-753-13
; Sequence 13, Application US/09904753
; Publication No. US20030092612A1
; Publication No. US20030092612A1
; GENERAL INFORMATION:
; APPLICANT: Lynos, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 23
                          TITLE OF INVENTION: Use of ANtimicrobal Peptides as Preservatives in TITLE OF INVENTION: Ophthalmic Preparations, Including Solutions, TITLE OF INVENTION: Emulsions, and Suspentions FILE REFERENCE: 2973 ver 2
CURRENT APPLICATION NUMBER: US/09/904,753
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: WO 96/25183
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 26
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Best Local 9
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LENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MCNICOL, PATRICIA J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE
TITLE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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TYPE: PRT
TYPE: PRT ORGANISM: Artificial Sequence
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Erfle, Douglas
Fraser, Janet R.
West, Michael H.P.
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; Pred. No. 0.0018;
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pred. No.
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. 0.0018;
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APPLICANT: PATRYKAT, Aleksander
APPLICANT: Woods, Donald
APPLICANT: Jia, Xiaoyan
TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICRO
TITLE OF INVENTION: PEPTIDES AND METHODS OF
FILE REFERENCE: 07422/016001
CURRENT APPLICATION NUMBER: US/09/908,139
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/143,124
PRIOR APPLICATION NUMBER: 09/143,124
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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COTHER INFORMATION:
COTHER INFORMATION:
US-09-904-753-13
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Best Local Similarity 85.7
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                                                                                                                                                                                                                                                                        Sequence 1, Application US/09908139 Publication No. US20030096949A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 120
LENGTH: 26
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
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APPLICANT: Krieger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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Erfle, Douglas
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Description of Artificial Sequence: Hybrid
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85.7%;
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Pred. No. 0.
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Pred. No. 0.002;
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CURRENT APPLICATION NUMBER: US/09/030,619B; CURRENT FILING DATE: 1998-02-25; SOFTWARE: Fastseq for Windows Version 3.0; SEQ ID NO 121; LENGTH: 28; TYPE: PRT
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APPLICANT:
                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                            APPLICANT: MCNICOL, PATRICIA J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALC TITLE OF INVENTION: WITH ANTIBIOTICS FIELE REFERENCE: 660081.406
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Best Local (
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                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/909,652
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/219,179
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Coleman, William J.
APPLICANT: Youvan, Douglas C.
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING
TITLE OF INVENTION: AND SCREENING COMPOUNDS THAT AFFECT CI
FILE REFERENCE: 22346-7001
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                                                                                                                                                                                          Taylor, Robert
Erfle, Douglas
Fraser, Janet R.
Fraser, Michael H.P.
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Pred. No.
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0.0022;
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; OTHER INFORMATION: Cationic Peptide Analogue US-09-030-619-121

ORGANISM: Artificial FEATURE:

Sequence

Matches

12;

Conservative

0;

Mismatches

Query Match Best Local Similarity

58.3%; 85.7%;

Score 63; DB 10; Pred. No. 0.0022;

Length 28

Indels

0;

Gaps

0;

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GENERAL INFORMATION:

APPLICANT: Owen, Donald R.

TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELX027

CURRENT APPLICATION UNMBER: US/09/820,053A

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 165

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 146

LENGTH: 23

TYPE: PRT
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; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-917-340-4
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                                 ; OTHER INFORMATION: AMIDATION US-09-820-053A-146
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                                                                                                                                                                                                                                                                                                                                                        Sequence 146, Application US/09820053A Publication No. US20030083243A1
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Murphy, Christopher J. APPLICANT: McAnulty, Jonathan F. APPLICANT: Reid, Ted W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR EILING DATE: 2000-11-17
                                                                     NAME/KEY: MOD_RES
                                                                                                         OTHER INFORMATION: SYNTHETIC SEQUENCE:
                                                                                                                          FEATURE:
                                                                                                                                           ORGANISM: ARTIFICIAL SEQUENCE
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     55.6%;
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     Score 60;
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US-09-908-139-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, App Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lynos, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: 1
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                                                                                                                                       LENGTH: 23
TYPE: PRT
ORGANISM: Xenopus laevis
PUBLICATION INFORMATION:
AUTHORS: Lee et al.,
                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local S
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TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR
FILE REFERENCE: 07422/016001
CURRENT APPLICATION NUMBER: 05/09/908,139
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/143,124
PRIOR APPLICATION NUMBER: 09/143,124
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Use of ANtimicrobal Peptides as Preservatives in TITLE OF INVENTION: Ophthalmic Preparations, Including Solutions, TITLE OF INVENTION: Emulsions, and Suspentions FILE REFERENCE: 2973 ver 2 CURRENT APPLICATION NUMBER: US/09/904,753 CURRENT FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hancock, Robert E. W. APPLICANT: Gough, Monisha A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Woods, Donald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: WO 96/25183
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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                 JOURNAL: Biochem. Biophys. Res. Commun. VOLUME: 277
PAGES: 575-580
                                                                           TITLE: High-Level Expression of Antimicrobal Peptide Mediated TITLE: by a Fusion Partner Reinforcing Formation of Inclusion TITLE: Bodies
DATE: Sept 21,
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12; Conserva
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No. US20030096949A1
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70.6%;
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1; Mismatches
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Pred. No. 0
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US-09-904-753-1

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CURRENT APPLICATION NUMBER US/09/030,619B
CURRENT ETLING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 210
LENGTH: 23
TYPE: PRT
ORGANISM: Xenopus laevis
US-09-030-619-210
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Search completed: June 6, 2003, 13:26:02 Job time: 15.5 secs
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7%;
Matches 11; Conservative
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APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Erfle, Douglas
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
APPLICANT: MCNicol, P
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1 GIGKFLHSAGKF 12
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Pred. No. 0.024;
0; Mismatches 1; Indels
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Pred. No. 0.024;
0; Mismatches 1; Indels
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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105
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992, DAT: *

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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994, DAT: *

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996, DAT: *

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999, DAT: *

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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
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Feige U, Liu C, Cheetham J, Boone TC;	(AMGE-) AMGEN INC.			23-OCT-1998; 98US-0105371.		25-OCT-1999; 99WO-US25044.		04-MAY-2000.		WOODDOO 180 - 30		Synthetic.	•	asthma; thrombosis; pharmaceutical.	vascular endothelial growth factor; matrix metalloproteinase;	cytotoxic T cell lymphocyte antiqen 4; tumour necrosis factor:	MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1:	immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagon(st.	autoimmune disease; cytostatic; antiasthmatic; thrombolytic: VEGF:	Modified peptide; therapeutic agent; fusion; Fc domain; cancer;	F-F College Care In 190. L. C.	Calmodulin antagonist peptide sequence SEO ID NO.179		31-OCT-2000 (first entry)		AAB17123;		AAB17123 standard; Peptide: 18 AA.	AAB17123	

Novel composition of matter comprising an pharmacologically active peptides, useful

Fc domain and
for treating cancer and

2000-350702/30

autoimmune diseases

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RESULT 2
ABB73201
ID 73201
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(X)a-Fl-(X2)b, where: Fl = an Fc domain; Xl and X2 = are each

cindependently selected from -(L1)c-Pl -(L2)d-P2.

-(L1)c-Pl-(L2)d-P2-(L3)e-P^3, or -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

where Pl, P2, P3, and P4 = are each independently sequences of

pharmacologically active peptides; Il, L2, L3, and L4 = are each

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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IGG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; II-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antiitumour; immunosuppressive; cytostatic; antiinfearmatory; antiinfertility; haemostatic; dermatological; antianaemic; anorectic; antiinfertility; haemostatic; dermatological; encuroprotective; inflammatory disease; autoimmune disease; tumour growth; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 39; Page 255; 608pp; English.
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Synthetic.
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    (AMGE-) AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67; DB 21 Pred. No. 0.03; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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The present invention describes a vehicle-peptide molecule (I) or its cultimers. (I) can have antiinflammatory, antitumour, immunosuppressive, conviously anorestic, antianthritic, antidiabetic, ophthalmological, contianemic, anorestic, antiinfertility, haemostatic, dermatological and concerning anorestic, antiinfertility, haemostatic, dermatological and concerning the properties of the control of the concerning purposes. (I) is useful for control of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their control of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, contentialty, and neurological degenerative diseases, (I), comprising compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful in thrombocytopaenia, systemic lupus erythematosus, and Fanconi's syndrome. ABB72403 to ABB73426 and ABI35695 to ABI35777 conditions that involve and actical actic actical acti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel vehicle-peptide molecule or its multimers useful for tree inflammatory and autoimmune diseases, cancer, rheumatoid arthridiabetic retinopathy, obesity, sleep disorders and infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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밁 δÃ Matches Query Match Best Local Similarity 16; ш Ν Conservative LLKKLLKKL 17 63.8%; 0; Score 67; I Pred. No. 0. 20 Mismatches DB .03; 23; 0; Length 18; Indels 4,

Sequence

18

AΑ;

exemplification of

the present invention.

RESULT 3 AAR21399 XX XXX DDE DE CONTROL AAR21399 standard; peptide; 16-MAY-1992 (first entry) 30

Sequence of amphiphilic peptide SEQ ID No. acetylated N-terminus, may be a C-terminal Amphiphilic spermicide; peptide; anti-microbial; anti-viral; anti-tumour; wound healing; sterilant.

62 with amide.

17-JUL-1991; 06-FEB-1992 19-ЈИГ-1990; WO9201462-A 90US-0554422 91WO-US05047

WPI; 1992-064700/08

RΑ,

Blondelle

(SCRI-) SCRIPPS RES INST.

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Best Local :
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The amphiphilic peptide (SEQ ID NO 62) was prepd. by standard solid phase methods. The peptide is an analogue of the peptide having SEQ ID NO 3 (AAR22824), with an N-terminal extension of 1 amino acids. Substitution and deletion analogues of this peptide
                                                               Claim
                                                                                         Amphiphilic peptide(s) and analogues - i
                                                                                                                                 WPI;
                                                                                                                                                                                                08-JUL-1991;
19-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptides of the invention are effective pharmaceuticals having anti-microbial, anti-viral and anti-tumour activity. They are also useful for inhibiting, preventing or destroying the motility of sperm and hence have application in a spermicide preparation. They also have anti-parasitic activity and are useful in wound healing, as preservatives and sterilants and to inhibit growth of phytopathogenic microorganisms. AAR20969 and AAR20970 were published in Haighten and Ostresh, Bio Chromatography, Vol 2, issue 2, page 80-83, near
                                                                                                                                                      Houghten
                                                                                                                                                                                                                                  18-JUL-1991;
                                                                                                                                                                                                                                                         20-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for inhibiting target cell and virus growth - comprises administering amphiphilic peptide compsns, useful for treating viral and phytopathogenic infections, tumours and burns
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                                                                                                                              1992-114943/15.
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                                                                                 biological activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                    Blondelle
                                                             60;
                                                                                                                                                                                               91US-0725331.
90US-0554442.
                                                                                                                                                                                                                                                                                                                                                                                       antifungal; antitumour; pharmaceuticals;
spermicides; burns; wound healing.
                                                                                                                                                                                                                                 91CA-2024317.
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                                                                                                      e.g.
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 peptide
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                                   Matches
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                                                                                                              anti-microbial, anti-viral and anti-tumour activity. They are also useful for inhibiting, preventing or destroying the motility of sperm and hence have application in a spermicide preparation. The also have anti-parasitic activity and are useful in wound healing, as preservatives and sterilants and to inhibit growth of phytopathogenic microorganisms. AAR20969 and AAR20970 were publish that they are also chromatography, vol 2, issue 2, page 80-
                                                                               Sequence
                                                                                                                                                                                         The peptides of the invention are effective pharmaceuticals having
                                                                                                                                                                                                                                         Method for inhibiting target cell and virus growth - administering amphiphilic peptide compsns, useful for viral and phytopathogenic infections, tumours and but
                                                                                                                                                                                                                    Disclosure; Page 61; 72pp; English.
                                                                                                                                                                                                                                                                                                                   Houghten RA,
                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           spermicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetylated N-terminus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               have increased biological activity and are effective as pharm ceuticals e.g. antibiotics for bacterial, fungal or viral infections, or in spermicides or antinuour or antiparasitic agents. Additionally the peptides can be used in wound healin compans. or for treating burns or other skin or eye infection can also antopaga-each
                                                                                                                                                                                                                                                                                                                                          (SCRI-) SCRIPPS RES INST.
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16; Conser
KWKKLLKKPPPLLKKLLKKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 AA;
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide; anti-m
wound healing;
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N-terminus, may be a
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                                                                               AA;
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80.0%;
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80.0%;
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Pred. No. 0.14
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                                                                                                            AAR20970 were published 2, issue 2, page 80-83,
                                                   Length 36;
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RESULT 6
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RESULT 7
AAR21398
ID AAR2
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Best Local S
Matches 16
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19-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphiphilic peptide(s) and analogues - i antimicrobial, antifungal or antitumour increased biological activity
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  Sequence of
                                                                                                 AAR21398
                                                 16-MAY-1992
                                                                                                                                                AAR21398 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 16; Conserv
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nilarity 80.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide to inhibit growth of a target cell.
  amphiphilic peptide
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                                                 (first entry)
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90US-0554442.
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36
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                                                                                                                                                                                                                                                                                                                                                               Score 64; DB
Pred. No. 0.14
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18-JUL-1991;

91CA-2024317.

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RESULT 8
AAR22882
ID AAR2
Query Match
Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for inhibiting target cell and virus growth - comprises administering amphiphilic peptide compsns, useful for treating viral and phytopathogenic infections, tumours and burns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amphiphilic peptide; anti-microbial; anti-viral; anti-tumour; spermicide; wound healing; sterilant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haighten
1987.
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                                                                                                                                                                                                                   antiparasitic;
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                                                                                                                 Modified-site
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Modified-site
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                                                                                                                                                                                                                                    Antimicrobial;
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                                          20-JAN-1992.
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                                                                                                                                                                                                                   antifungal; antitumour; pharmaceuticals;
spermicides; burns; wound healing.
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83.3%;
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                                                                                                     "amidated
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                                                                                                                                "acylated"
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issue 2, page 80-83,
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RESULT 9
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                                                            New conjugates of bioactive amphiphilic peptide(s) moiety - are useful for treatment of septic shock
               Disclosure; Page 120; 141pp; English
                                                                                                                                                                                                                                                   (MAGA-)
                                                                                                                                                                                                                                                                                                   07-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                     06-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09413697-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gram negative bacterial endotoxin; lipopolysaccharide; LPS; gram negative bacteria; conjugate moiety; septicemia; neutralising; longer activity; polyvinylpyrrolidone; dextran; hetastarch; polyvinyl alcohol; ion-channel forming.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The amphiphilic peptide (SEQ ID NO 61) was prepd. by standard solid phase methods. The peptide is an analogue of the peptide having SEQ ID NO 3 (AAR22824), with an N-terminal extension of 8 maino acids. Substitution and deletion analogues of this peptide have increased biological activity and are effective as pharmacuticals e.g. antibiotics for bacterial, fungal or viral infections, or in spermicides or antitumour or antiparasitic agents. Additionally the peptides can be used in wound healing compsns. or for treating burns or other skin or eye infections. See also AAR22822-89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR56957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide which neutralises bacterial endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amphiphilic peptide(s) and analogues - antimicrobial, antifungal or antitumous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increased biological activity
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19-JUL-1990;
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antifungal or antitumour compositions, having
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90US-0554442.
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Pred. No.
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Best Local
The present invention describes a method for producing micelles with entrapped therapeutic agents. The method comprises: (1) combining negatively charged agent with a cationic lipid in a ratio where 30-90 % of the negatively charged atoms are neutralised by positive charges on lipid molecules to form an electrostatic micelle complex in 20-80 % ethanol; and (2) combining the micelle complex of (a) with fusogenic-karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing micelles with entrapped therapeutic agents. Also described is a method for delivering a therapeutic agent in vivo, comprising the administration of the micelle. ABB74256 to ABB74858 represent specifically claimed nuclear localisation signal (NLS) peptides for use in the method as the fusogenic-karyophilic peptides. The micelles produced can have cytostatic and antitumour activities.
                                                                                                                                                                                                                                                                              Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with nuclear localization signal/fusogenic peptide conjugates into targeted
                                                                                                                                                                                                                                                                                                                                          WPI; 2002-164295/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Septic shock is often due to the body's reaction to foreign lipopolysaccharide (LPS). The compounds of the invention neutralise bacterial endotoxins without neutralising essential proteins in the plasma of patients, eg.heparins. They also have longer duration of activity than unconjugated peptides. In general peptides such as this are ion-channel forming peptides. The compounds are biologically active peptides linked to a conjugate moiety, eg. carbohydrates, proteins, polyvinylpyrrolidone, polyalkylene glycols and polyvinyl alcohols. The conjugate moiety may be linked at the C- or N-terminal or internally of the peptide. ARR55591-631 and ARR56879-957 are examples
                                                                                                                                                                                                                                       Example; Page 38; 107pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUN-2000; 2000US-210925P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene; liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour; peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy; breast carcinoma; prostate carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-2001; 2001WO-US18657.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                           Liposome
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                                                                                                                                                                                                                                       English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
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                                                                                                                                        The present peptide is a specific example of a cationic oligopeptide corresp. to the formula (b-1-1-b)n, where b is a hydrophobic amino acid 1 is a hydrophilic amino acid and n is at least 4. In this case, where b is Leu, 1 is Lys and n = 10, the oligopeptide forms an alpha-helix which forms a stable complex with a nucleic acid. The complex is suitable for transferring nucleic acid, esp. in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                  Complex of nucleic acid and oligopeptide with sec. structure transfer vectors contg. them, useful for efficient transfer concleic acid to cells in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-1994;
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                                                                                                                                                                                                                                                                                                                      Claim 6 and
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al Similarity
15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 AA;
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                                                                                                                                                                                                                                                                                                                        Example 1.1;
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     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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83.3%;
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                                                                                                                                                                                                                                                                                                                           Page 7; 20pp;
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08-FEB-1990;
14-MAY-1990;
28-APR-1992;
17-NOV-1994;
                                                                                                                           The invention relates to analogues of a magainin I or II, D-form analogues, deletion analogues or related peptides. It also relates to basic polypeptides having at least 16 amino acids, including at 18 hydrophobic amino acids and at least 8 hydrophilic amino acids. The peptides may be used as antimicrobial agents, antiviral agents, antipiotics, antitumour agents, antiparasitic agents, spermicides, preservatives or sterilants, or agents for promoting wound healing. present sequence represents a specific example of a peptide disclose the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW66517;
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                                                                                                                                                                                                                                                                                       Maloy WL;
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                                                                                                                                                                                                                         Disclosure; Column
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                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                           93US-0133740.
90US-0476629.
90US-0522688.
92US-0874685.
94US-0343882.
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                                                                                                                                                                                                                                                   analogues -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antimicrobial; antitumour; wound healing;
                                       -LKKLLKKL
                                                                                   52.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide.
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pred. No. 0.96
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                                                                                                                                                                                                                                                     useful as antimicrobial or antitumour
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AAR21385 standard;

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RESULT 14
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Best Local
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                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                    Antimicrobial; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The peptides of the invention are effective pharmaceuticals having anti-microbial, anti-viral and anti-tumour activity. They are also useful for inhibiting, preventing or destroying the motility of appear and hence have application in a spermicide preparation. They also have anti-parasitic activity and are useful in wound healing, as preservatives and sterilants and to inhibit growth of phytopathogenic microorganisms. AAR20969 and AAR20970 were published haighten and Ostresh, Bio Chromatography, Vol 2, issue 2, page 80-83, nag
                                                                                  Modified-site
                                                                                                                                                                                                                                             Amphiphilic peptide to inhibit growth of a target cell.
                                                                                                                                                                                                                                                                                                                                                    AAR22869 standard; Peptide;
                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                        22-AUG-1992
                                                                                                                                                                                                                                                                                                                          AAR22869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for inhibiting target cell and virus growth - comprises administering amphiphilic peptide compsns, useful for treating viral and phytopathogenic infections, tumours and burns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of amphiphilic peptide SEQ ID No. 48 C-terminal amide and acetylated at N-terminus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 54; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AA;
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                                                                                                                                                                                                                                                                                  (first entry)
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17
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                                                                                                                                                                                                    spermicides;
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75.0%;
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burns; wound healing.
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Query Match
Method for inhibiting target cell and virus growth - administering amphiphilic peptide compsns, useful for viral and phytopathogenic infections, tumours and bur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              solid phase methods. The peptide is an analogue of the peptide having SEQ ID NO 3 (AAR22824), with Leu at position 4 deleted. Substitution and deletion analogues of this peptide horeased biological activity and are effective as pharmaceuticals e.g. antibiotics for bacterial, fungal or viral infections, or in the peptides or antitumour or antiparasitic agents. Additionally burns or other skin or eye infections.
                                                                                                                                                                                                                                                                                                                          Amphiphilic spermicide;
                                                                               WPI; 1992-064700/08.
                                                                                                                                                                                                                                                         06-FEB-1992
                                                                                                                                                                                                                                                                                           W09201462-A
                                                                                                                                                                                   19-JUL-1990;
                                                                                                                                                                                                                      17-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                       Sequence of amphiphilic peptide SEQ ID Nerminal amide and/or may be acetylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR21360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR21360 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 54; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amphiphilic peptide(s) and analogues - for use in e.g. antimicrobial, antifungal or antitumour compositions, having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increased biological activity
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19-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLKKLLKK----LKKLLKKL 17
                                                                                                                                                                                                                                                                                                                     peptide; anti-microbial; anti-viral; anti-tumour;
wound healing; sterilant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                               Blondelle
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90US-0554442
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75.0%;
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N-terminus.
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                  for treating
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burns

Claim 4; Page 42; 72pp; English.

XX

The peptides of the invention are effective pharmaceuticals having cc anti-microbial, anti-viral and anti-tumour activity. They are also completed: John the motality of cc anti-microbial, anti-viral and anti-tumour activity. They are also need in the motality of cc also have anti-parasitic activity and are useful in wound healing, cc phytopathogenic microorganisms. ARR20969 and ARR20970 were published in cc phytopathogenic microorganisms. ARR20969 and ARR20970 were published in cc ladghten and ostresh, Bio Chromatography, Vol 2, issue 2, page 80-83, cc 1987.

XX

Sq Sequence 18 AA;

Query Match

Scala; Score 55; DB 13; Length 18;

Best Local Similarity 77.8%; Pred. No. 1.1;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Scarch completed: June 6, 2003, 13:23:39

Job time: 31.5 secs

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OM protein -
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Perfect score:
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Listing first 45 summaries
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Maximum DB
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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        6, 2003, 13:22:11; Search time 12.5 Seconds
(without alignments)
153,815 Million cell updates/sec
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calpain (EC 3.4.22
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gag protein - maiz
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   probable ATP-depen
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## ALIGNMENTS

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Ţ	ion: 3 8/3; 593/3 9021.110	A;Molecule type: DNA A;Residues: 1-900 <bnd:atf18021 A;Cross-references: EMBL:ATF18021 A;Experimental source: cultivar Columbia; BAC clone F18021 C:Genetics:</bnd:atf18021 	C;ACCESTON: 17/02 R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, f submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24474 A;Accession: T47732 A;Status: preliminary	nslation initiation factor eIF-3 chain 8 F18O21.110 [imported] - Arabido rabidopsis thaliana (mouse-ear cress) pr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000	QY 1 KWKKLLKKPPPLLKKLLKKL 20  : :  :    :       12 KFKRLLQLPPPAFANILKIL 39	Query Match 48.6%; Score 51; DB 2; Length 369; Best Local Similarity 50.0%; Pred. No. 11; Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;	C;Genetics: A;Gene: CESP:T10C6.7 A;Map position: 5 A;Introns: 44/2; 114/2; 219/3; 313/2 C;Superfamily: Caenorhabditis elegans hypothetical protein F08F3.6	A; Experimental source: clone T10C6  A; Experimental source: clone T10C6	A; Reference number: 219936 A; Accession: T24797 A; Status: preliminary; translated from GB/EMBL/DDBJ	R;McMurray, A. submitted to the EMBL Data Library, March 1997	C;Species: Caenormauditis eregums C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000 C:Accession: T24797	RESULT 1 T24797 Typothetical protein T10C6.7 - Caenorhabditis elegans hypothetical protein F10C6.7 - Caenorhabditis elegans

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A;Title: The genome sequence of the A;Reference number: A81250; MUID:201 A;Accession: E81331
                                                                    A;Status: preliminary
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A;Residues: 1-110 <AYR>
A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66737.1; PID:g559176
                                                                                                                                                                                                                                                                                                                                                                                                                        R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: D72863
                                                                                                                                                                                                                                                                                                                                                    A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C;Accession: D72863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Karniol, B.; Yahalom, A.; Kwok, S.; Tsuge, T.; Matsui, M.; Deng, X.W.; Chamovitz, D.A. FEBS Lett. 439, 173-179, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation initiation factor homolog p105 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: T50773
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Best Local
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                           e of the food-borne pathogen Campylobacter jejuni reveals wUID:20150912; PMID:10688204
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A; Residues: 1-656 < DIE>
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S69554
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C;Superfamily: uroporphyri
C;Keywords: carbon-carbon
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A;Molecule type: mRNĀ
A;Residues: 1-1235 <DAV>
A;Cross-references: EMBL:X60421; NID:g1657;
C;Keywords: liver; phosphotransferase
                                                                                                                                                                                                               R;Davidson, J.J.; Dezcelik, T.; Hamacher, C.; Willems, P.J.; Francke, U.; Kilimann, Proc. Natl. Acad. Sci. U.S.A. 89, 2096-2100, 1992
A;Title: cDNA cloning of a liver isoform of the phosphorylase kinase alpha subunit A;Reference number: S24109; MUID:92196064; PMID:1372435
A;Accession: S24109
                                                                                                                                                                                                                                                                                                             C;Species: Oryotolagus cuniculus (domestic rabbit)
C;Decies: Oryotolagus cuniculus (domestic rabbit)
C;Date: 25-Feb-194 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: S24109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: SGD:PUF6; MIPS:YDR496c
A;Cross-references: SGD:S0002904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, August 1995
A;Description: The sequence of S. cerevisiae cosmids 8166, 9787,
A;Reference number: S69553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U33057; NID:g927764; PID:g927766; GSPDB:GN00004; MIPS:YDR496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein YDR496c - yeast (Saccharomyces C;Species: Saccharomyces cerevisiae C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-340 <PAR>
A; Cross-references: GB: AL139077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:AL139077; GB:AL111168; NID:96968444; PIDN:CAB73497.1; PID:9696
Experimental source: serotype O2, strain NCTC 11168
5 LLKKPPPLLKKLLKKL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 KCKKMLYONPELLHKILNKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 WKKLLKKPPPLLKKLLKKL 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WERLRVKTPPLPKQIREKL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uroporphyrinogen decarboxylase
rbon-carbon lyase; carboxy-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
                                                        46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.78;
47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.7%;
55.0%;
                                        4.
                                                    Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 37;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49;
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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. No. 19;
                                                  DB
. 71;
                                                                                                                            PIDN:CAA42952.1; PID:g1658
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37;
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                                  Ψ
                                                                     Length 1235;
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                            Gaps
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                              0;
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A.Description: catalyzes the hydolysis of peptides A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and before c.Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain c.Keywords: acetylated amino end; calcium binding; cysteine proteinase; EF hand; heterographic calpain large chain 2 #status predicted <MAT>
                                                                                                                                                                                                                F;2-700/Product: calpain large chain 2 #status prec
F;75-327/Domain: calpain catalytic domain homology
F;529-560/Domain: calmodulin recent homology
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:CAPN2; mCANP; CANPml
A;Cross-references: GDB:119750; OMIM:114230
A;Map position: lpter-lqter
C;Complex: heterodimer of L (large) and S (small) chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA; protein
A;Residues: 1-210,'I','212-394,'D','396-445,'I',447-700 <IMA>
A;Residues: 1-210,'I','212-394,'D','396-445,'I',447-700 <IMA>
A;Residues: 1-210,'I','212-394,'D','396-445,'I',447-700 <IMA>
A;Ross-references: GB:M23254; NID:g511637
A;Note: parts of this sequence were determined by protein sequencing; the amino end R;HAtta, A.; Ohno, S.; Akita, Y.; Suzuki, K.

J. Biol. Chem. 264, 6404-6411, 1989
A;Title: Tandemly reiterated negative enhancer-like elements regulate transcription
A;Reference number: A33529; MUID:89197947; PMID:2539381
A;Accession: A33529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-67,'G',69-72,'IE',75-78,'R' <HAT>
A;Cross references: DDBJ:J04700; NID:g179910; PIDN:AAA52760.1; PID:g463086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-700 <SOR>
R;Imajoh, S.; Aoki, K.; Ohno
Biochemistry 27, 8122-8128,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 09-Aug-1997 #text_change 16-Jul-1999
C:Accession: S10590; A31218; A33529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Molecular cloning of the cDNA for the large subunit of A;Reference number: A31218; MUID:89166474; PMID:2852952 A;Accession: A31218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Sorimachi, H.; Ohmi, S.; Emori, Y.; Kawasaki, H.; Saido, T.C.; Ohno, S.; Biol. Chem. Hoppe-Seyler 371(Suppl.), 171-176, 1990
A;Title: A novel member of the calcium-dependent cysteine protease family.
A;Reference number: S10589; MUID:90380278; PMID:2400579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calpain (EC 3.4.22.17) large chain 2 - human
N;Alternate names: calpain chain L-2; calpai
                                              ;529-560/Domain: calmodulin repeat homology <EFT>;572-604/Domain: calmodulin repeat homology <EFT>;605-634/Domain: calmodulin repeat homology <EFT>;605-634/Domain: calmodulin repeat homology <EFT>;637-669/Domain: calmodulin repeat homology <EFT>;2/Modified site: acetylated amino end (Ala) (in mature;105,262,286/Active site: Cys, His, Asn #status predicte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S10590
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A; Residues: 1-668 <CAP>
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Cell 43, 105-115, 1985
A;Title: Sequence of Dictyostelium DIRS-1: an apparent retrotransposon with inverted A:Reference number: A94654; MUID:86079481; PMID:2416457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Dictyostelium discoideum C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 18-Jun-1993 C:Accession: C24785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cappello,
Cell 43, 10
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C;Species: Dictyostelium
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   Score 48.5;
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Pred. No. 4
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                                                 #status predicted
   DВ
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                                                                               #status
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Length 700

Nature

R; Tomb,

C;Date: 09-Aug-1997 #sequence\_revision C;Accession: D64595

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,

McKe

uroporphyrinogen decarboxylase - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori

09-Aug-1997

#text\_change

22-Jun-1999

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A;Varrety: Security sequence_revision 14.500.

C;Date: 12-Feb-1999 #sequence_revision 14.500.

C;Accession: E71918

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, (Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastria: A:Reference number: A71800; MUID:99120557; PMID:9923682
RESULT 12
D64595
                                                                                                                                                                                                                  C; Superfamily:
                                                                                                                                                                                                                                                     A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-339 <ARN>
                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE001487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Lee, J.H.; Lee, M.S.; Chen, K.T.; Chang, G.D.; Chou, C.K.; Huang, C.J.
Biochim. Biophys. Acta 1306, 133-136, 1996
A; Title: Genomic structure of carp mitogen-activated protein kinase kinase 1 gene.
A; Reference number: S70028; MUID:96221282; PMID:8634328
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S70028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Variety:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uroporphyrinogen decarboxylase -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitogen-activated protein kinase kinase 1 - common carp (fragments) C;Specites: Cyprinus carpio (common carp) C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 17-Mar-1999 C;Accession: S70028
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R; Leu, J.H.; Lee,
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                                                                                                                                                            Query Match
Best Local
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Best Local
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                                                                                                                                                            Similarity
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                                                                 KSKKMLYSEPEVLKALLEKL 178
                                                                                                  KWKKLLKKPPPLLKKLLKKL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVNEPPPVMKCLMKKM
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                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                     strain
                                                                                                                                                          45.7%;
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                                                                                                                                                                                                                                                                            GB:AE001439; NID:g4155086; PIDN:AAD06123.1;
                                                                                                                                       ω,
                                                                                                                                                        Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 46;
5; Mismatches
                                                                                                                                     Mismatches
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-340 <TOM>
A; Cross-references: GB: AE000574; GB: AE000511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: A81707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-dependent Clp proteinase, chain B TC0389 [imported] - Chlamydia muridar C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001 C:Accession: A81707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: endopeptidase Clp ATP-binding chain C;Keywords: ATP; molecular chaperone; nuclectide binding; F;205-212/Region: nucleotide-binding motif A (P-loop) F;273-278/Region: nucleotide-binding motif B F;605-612/Region: nucleotide-binding motif A (P-loop) F;673-678/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-867 <TET>
A;Cross-references: GB:AE002306; GB:AE002160; NID:g7190428; PIDN:AAF39246.1;
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                             cell proliferation antigen Ki-67, short form - human
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;211/Binding site: ATP (Lys) #status predicted F;611/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A;Molecule type: mRNA
A;Residues: 1-2897 <SCH>
A;Cross-references: EMBL:X65551
C;Superfamily: kinase interaction
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                                                                                                                 A;Reference number: A48666; MUID:94043435; PMID:8227122 A;Accession: B48666
                                                                                                                                                                                    A; Title: The cell proliferation-associated antigen of antibody Ki-67: a very
                                                                                                                                                                                                             C;Accession: B48666
R;Schlueter, C.; Duchrow, M.; Wohlenberg,
J. Cell Biol. 123, 513-522, 1993
                                                                                         A; Status: preliminary
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Best Local
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKKLLKKPPPLLKKLLKKL 20
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llarity 47.4%;
Conservative
       interaction
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Pred. No. 68;
4; Mismatches
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Pred. No. 26;
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         domain homology
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    Chlamydia muridarum (strain

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Search completed: Job time : 14.5 se

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A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-3256 <SCH>
A;Residues: 1-3256 <SCH>
A;Cross-references: EMBL:X65550; NID:g415818; PIDN:CAA46519.1;
A;Cross-references: EMBL:X65550; NID:g415818; PIDN:CAA46519.1;
C;Superfamily: kinase interaction domain homology
C;Superfamily: kinase interaction domain homology <KIH>
C;KeywordS: alternative splicing; cell cycle control; nucleus;
C;KeywordS: alternative interaction domain homology <KIH>
C;KeywordS: Area and A
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A48666
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Best Local Similarity
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R;Schlueter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, J. Cell Biol. 123, 513-522, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell proliferation antigen Ki-67, long C: Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A48666
                                                                          Query Match
Best Local S
Matches 9
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                                                                                  9;
                                                                                                                         Similarity
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KWKKLLKKPPPLLKKLLKK 19
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Pred. No. 2.4e+02;
                                                                                           Score 48; DB 2; pred. No. 2.7e+02; Signatches 5;
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Minimum DB :
Maximum DB :
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Maximum Match 100%
Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      BLOSUM62
Gapop 10.0 , Gapext 0.5
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133.213 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
/cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep: *
/cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep: *
/cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep: *
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US-09-99-745-52
US-09-99-745-53
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US-09-80-053A-49
US-09-80-053A-49
US-09-80-053A-69
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US-09-864-761-40695
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                          Sequence 2, Appli
Sequence 629, Appl
Sequence 629, Appl
Sequence 39, Appl
Sequence 1, Appl
Sequence 125, Appl
Sequence 49, Appl
Sequence 56, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 98, Appl
Sequence 98, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
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US-10-081-418-2
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HAHM, Kyung-Soo
APPLICANT: LEE, Dong Gun
APPLICANT: PARK, YoonKyung
APPLICANT: PARK, YoonKyung
APPLICANT: KIM, Hee Nam
TITLE OF INVENTION: NO. US20030096745Alel peptides with increased +
TITLE OF INVENTION: substituting one or more amino acids of CA-MA p
TITLE OF INVENTION: pharmaceutical compositions containing thereof
FILE REFERENCE: 428.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10081418 Publication No. US20030096745A1
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41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	42.4	42.4	42.9	42.9	42.9
491	491	489	242	216	26	26	23	23	940	907	907	779	598	529	529	242	67	23	22	22	610	20	510	510	74
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US-09-888-077-1	US-09-029-327-2	US-09-956-425-6	US-09-764-898-199	US-10-057-510-4	US-09-030-619-122	US-09-908-139-2	US-09-820-053A-161	US-09-820-053A-9	US-10-102-806-678	US-09-954-043-4	US-10-200-154-4	US-10-060-019-29	US-09-925-301-1218	US-10-051-909-28	US-10-051-902-28	US-09-764-853-609	US-09-843-845-17	US-09-820-053A-55	US-09-820-053A-48	US-09-820-053A-46	US-09-738-626-4495	US-09-820-053A-68	us-10-051-909-22	US-10-051-902-22	US-09-864-761-33838
,		Sequence 6, Appli	Sequence 199, App	Sequence 4. Appli	e 12	2	161	Sequence 9. Appli	Sequence 678. App	Ф 4	Sequence 4, Appli	Sequence 29, Appl	Sequence 1218, Ap	Sequence 28, Appl	Sequence 28, Appl	ō.	Sequence 17, Appl	55	48		۰ 4	68	Sequence 22. Appl	Sequence 22, Appl	Sequence 33838. A

## ALIGNMENTS

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RESULT 2
US-09-876-904A-15
; Sequence 15, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PI
                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: peptide with increased + charge and hydrophobicity by ; OTHER INFORMATION: substituting amino acids of SEQ. ID. NO 1 with lysine and US-10-081-418-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/081,418
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: KOPAtentin 1.71
SEQ ID NO 2
LENGTH: 20
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                            1 KWKKLLKKPPPLLKKLLKKL
                                                                                                                                                                                                                                                                                         20;
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                                                                                                                                                                                                                                                                                   100.0%; Score 105; DB 9; ilarity 100.0%; Pred. No. 1.7e-07; Conservative 0; Mismatches 0;
           ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
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Sequence 629, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                  RESULT 4
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 629
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                                                                                                                                                                         Sequence 55, Application US/09999745 Patent No. US20020157120A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                APPLICANT: Tsien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                    APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic amphiphilis OTHER INFORMATION: fusogenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                          53.8%;
83.3%;
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Pred. No. 0
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Pred. No. 0.
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; OTHER INFORMATION: Calmodulin binding peptide-2 US-09-999-745-55
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US-09-554-000-39
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NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.0
SEQ ID NO 55
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/554,000
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 08/818,252
PRIOR FILING DATE: 1997-03-14
                                 APPLICANT: Monahan, Sean D
APPLICANT: Slattum, Paul M
APPLICANT: Slattum, Paul M
APPLICANT: Hagstrom, James E
APPLICANT: Hagstrom, James E
APPLICANT: Rozema, David B
TITLE OF INVENTION: INTERAVASCULAR DELIVERY OF NON-VIRAL NUCLEIC ACID
FILE REFERENCE: Mirus.013.03
FILE REFERENCE: Mirus.013.03
CURRENT APPLICATION NUMBER: US/09/447,966
CURRENT FILING DATE: 1999-01-23
PRIOR APPLICATION NUMBER: 60/121730
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: MIYAwaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
                                                                                                                                                                                                                         APPLICANT:
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PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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     1999-07-30
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76.5%;
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76.5%;
                     60/146564
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Pred. No. 0.75;
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Pred. No. 0
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                                                                                                                                                                                                                                                US-09-820-053A-49
                                                                        CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2001-0
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 125
LENGTH: 26
                                                                                                                                                                                                 Sequence 49, Application US/09820053A Publication No. US20030083243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                     TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES FILE REFERENCE: HELX027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
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                                                                                                                                                                                      APPLICANT: Owen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT: MCNLOO1, Patricia J.
TILE OF INVENTION: COMPOSITIONS AND
TILE OF INVENTION: INFECTIONS USING
TILE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
OTHER INFORMATION: SYNTHETIC SEQUENCE
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                            RGANISM: ARTIFICIAL SEQUENCE
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nes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser, Janet R.
West, Michael H.P.
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76.5%;
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Pred. No.
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Pred. No. 3.8;
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CATIONIC PEPTIDES AL
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Best Local Similarity
Matches 12; Conserv
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LENGTH: 23
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
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Best Local
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CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/562,979
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/198,210
PRIOR FILING DATE: 1999-04-27
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/038,557A
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION UNMBER: 09/840,707
PRIOR FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fredeking, Terry M. APPLICANT: Ignatyev, George M.
                               OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS FILE REFERENCE: 24881-301D
                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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PATENT FILING DATE:
PATENT DOCUMENT NUMBER: 5,817,476
PATENT FILING DATE: 1995-06-07
                                                                                                                                          ENGTH: 700
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Pred. No. 3.9;
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Patent No. U
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                                                     APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT.OF TYPE 2 DIABETES
FILE REFERENCE: ARCD:307
CURRENT APPLICATION NUMBER: US/09/768,877
CURRENT FILING DATE: 2001-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS FILE REFERENCE: 24881-301C CURRENT APPLICATION NUMBER: US/09/840,707A CURRENT FILING DATE: 2001-04-23 PRIOR APPLICATION NUMBER: 09/562,979 PRIOR APPLICATION NUMBER: 09/562,979 PRIOR FILING DATE: 2000-04-27 PRIOR PILING DATE: 2000-04-27 PRIOR FILING DATE: 1999-04-27
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION: PATENT DOCUMENT NUMBER: 5,817,476 PATENT FILING DATE: 1995-06-07 PUBLICATION DATE: 1998-10-06
 PRIOR APPLICATION NUMBER: 09/422,869
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fredeking, Terry M. APPLICANT: Ignatyev, George M.
                                                                                                                                                                                                                                                              APPLICANT: POLONSKY, KENNETH S. APPLICANT: HORIKAWA, YUKIO
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TYPE: PRT
ORGANISM: Homo sapiens
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COX, NANCY J.
SREENAN, SEAMUS
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Pred. No. 1.
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Pred. No. 1.
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US-10-051-909-20
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; ORGANISM: Human
US-09-768-877-23
                                        US-10-051-909-20
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LENGTH: 513
TYPE: PRT
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                                                                                                             SEQ ID NO 20
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Best Local :
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                                                                                                                                                          APPLICANT: Kinney, Tony
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB1163 US CIP
CURRENT APPLICATION NUMBER: US/10/051,909
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 60/083,044
PRIOR FILING DATE: APPLI 24, 1998
PRIOR FILING DATE: APPLI 24, 1998
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TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB-1163
CURRENT APPLICATION NUMBER: US/10/051,902
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/291,922
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 30
                                                                                                                               NUMBER OF SEQ ID NOS: SOFTWARE: Microsoft O
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APPLICANT:
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                                                       ORGANISM: Zea mays
                                                                           TYPE: PRT
                                                                                          LENGTH: 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 EWYE-LKKPPPNLFKIIQK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 WKKLILSPTPAVRRIL 282
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7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allen, Steve
Hitz, Bill
Kinney, Tony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WKKLLKKPPPLLKKLL 17
                                                                                                                                                                                                                                                                                                                    Helentjaris,
Hitz, Bill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.7%;
milarity 43.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                        Steve
                                                                                                                                  Office 97
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52.6%;
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Pred. No. 1.2e
5; Mismatches
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Pred. No.
 Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
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 9;
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Length 513;
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Indels

0;

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밁

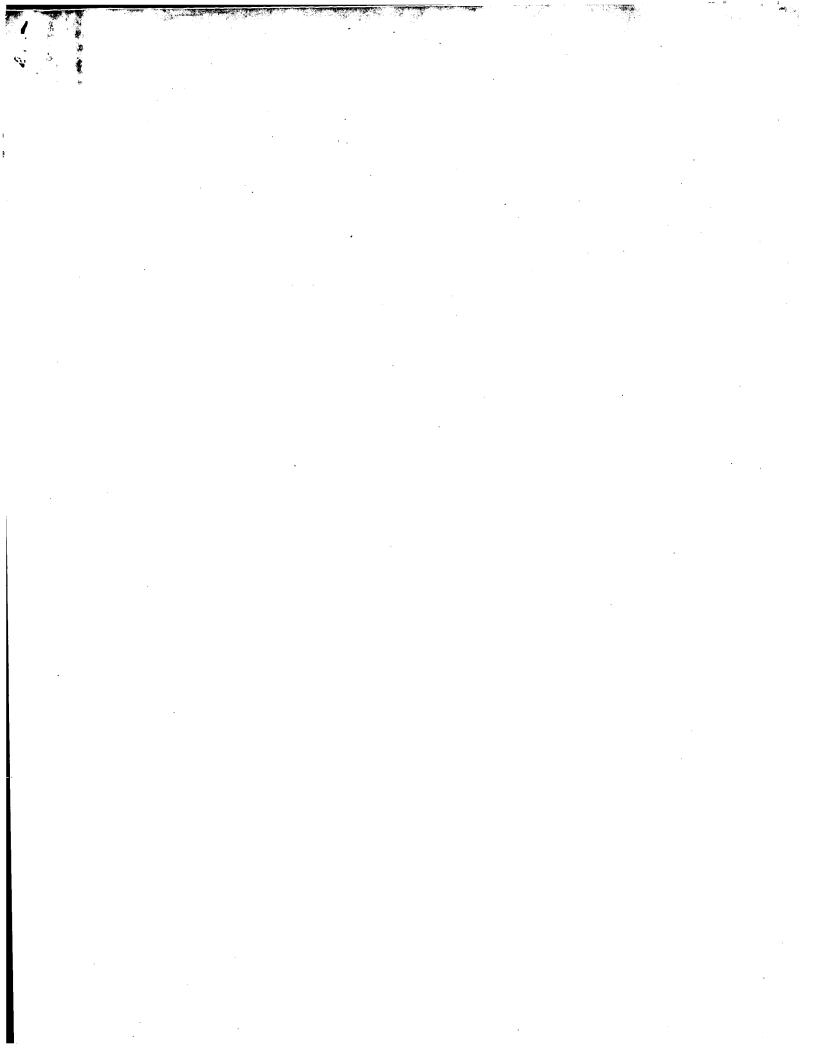
```
Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 WKKLIKRPPDLKKLL 17

Db 267 WKKLILSPTPAVRKIL 282

RESULT 15

US-09-919-172-98
: Sequence 90, Application US/09919172
: Patcht No. US20020119463A1
: GENERAL INFORMATION:
: APPLICANT: Furier, Christopher M.
: TITLE OF INVENTION: PROSPATE CANCER MARKERS
: FILE REFERENCE: PA-0035 US
: CURRENT FILING DATE: 2001-07-29
: PRIOR APPLICANTION NUMBER: US/09/919,172
: CURRENT APPLICANTION UNBER: US/09/919,172
: CURRENT APPLICANTION UNBER: US/09/919,172
: CURRENT APPLICANTION UNBER: US/09/919,172
: PRIOR APPLICANTION UNBER: US/09/919,172
: CURRENT APPLICANTION UNBER: US/09/919,172
: PRIOR APPLICANT
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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
               Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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105
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45.00.05
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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          357
173
341
369
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700
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1110
          5 09GRQ3
16 08YMP7
5 045769
15 09GP16
5 09GP1
16 09PN54
5 09G84
5 096849
5 093898
4 099BB1
4 08WU26
6 09GLG1
11 09PKS5
15 09WCA9
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Oggrq3 leishmania
Ogfjp3 arabidopsis
OBxmh7 clostridium
O45769 caenorhabdi
Og9lym6 arabidopsis
Oggq51 dictyosteli
Oggn54 campylobact
O4373 saccharomyc
C96849 dictyosteli
O23898 dictyosteli
O39801 homo sapien
O89026 homo sapien
O89026 dictyosteli
O23898 dictyosteli
O39802 dictyos
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4.5	44	4	4.2	41	40	9	8	37	36	35	34	ω ω	3.2	ω 1	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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42.9		42.9				42.9	٠					43.3	ω	43.8					43.8					43.8	44.3	44.8	44.8	44.8
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w	drosophila	plutella	Q9xej2 zea mays (m		$\sim$	ب	Q39352 brassica na	LΠ		3		ø			to	mus mu	turkey	-		Q9fp52 oryza sativ	Q9vd68 drosophila			N	Q.		īmg2 arabid	Q9ylfl human immun

## ALIGNMENTS

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4 KLLKKPPPLLKKLLKK 19          85 KLLKKPPPTFTLLMKR 100	Query Match 50.5%; Score 53; DB 5; Length 357; Best Local Similarity 62.5%; Pred. No. 9.1; Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	Hypothetical protein. SEQUENCE 357 AA; 39621 MW; D27C03EFF2B2139E CRC64;	"A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998). EMBL; AL446005; CAC14538.1;	Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;	6435;	SEQUENCE FROM N.A.	[2]	Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.	Patrician V., Furnette B., Golleau A., Ivens A.C., Quail M.,		SEQUENCE FROM N.A.		במאמנן פרם, במקופוטבטם; אוופרטפומצרוטם; Trypanosomatidae; Leisnmania. NCBI_TaxID=5664;	major.		cal 39.6 kDa protein.	(TremBirel. 16, Last annotation	(TrEMBLrel. 16,	01-MAR-2001 (TremBLrel. 16, Created)	Q9GRQ3;	Q9GRQ3 PRELIMINARY; PRT; 357 AA.	LT 1 03

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RESULT
Q8XMH7
Q8XMH7
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Best Local S
Matches 10
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"Full Length cDNA of gene MQN23.16/AT5g65220 (GI:10178184).";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ datahaaco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9FJP3;
Q9FJP3;
Q1-MAR-2001
                                                                                       Q8XMH7
Q8XMH7;
Q1-MAR-2002
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Q1-MAR-2002
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Hypothetical protein CPI
CPE0712.
Clostridium perfringens.
Bacteria; Firmicutes; Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Southwick A., Davis R.W., Ecker J.R., Theologis A.;
"Arabidopsis Open Reading Frame (ORF) Clones.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB013395; BAB11558.1;
EMBL; AY045966; AAK76640.1;
EMBL; AY079351; AAL85082.1;
EMBL; AY079351; AAL85082.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana of Sequence features of the regions of 1,367,185 physically assigned Pl and TAC clones."; DNA Res. 5:203-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AT5G65220
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98403884; PubMed=9734815; Kotani H., Nakamura Y., Sato S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-COLUMBIA;
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TIGRFAMS; TIGR00012; L29; 1
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173 AA;
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(TremBLrel. 16, Last sequence up,
(TremBLrel. 21, Last annotation
                                                               2 (TrEMBLrel. 20, C)
2 (TrEMBLrel. 20, La
2 (TrEMBLrel. 20, La
11 protein CPE0712.
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  Bacillus/Clostridium
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ribosomal protein
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Karlin-Neumann
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    Clostridia;
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RESULT
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STRAIN=13 / TYPE A;
PubMed=11792842;
Shinizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashi
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi
Shiba T., Ogasawara Sequence of Clostridium perfringens, a
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01-JUN-1998
01-DEC-2001
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045769;
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NCBI_TaxID=1502;
OPLYM6:
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable eukaryotic translation initiation factor 3 subunit 8
(Putative eukaryotic translation initiation factor 3 subunit F18021_110 OR AT3G56150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
NCBI_TaxID-6239;
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Science 282:2012-2018(1998).
EMBL; Z93388; CAB07663.1; -.
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AP003187; BAB80418.1; -
hetical protein; Complete
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369 AA; 43506 MW;
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Caenorhabditis.
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Q9GQ51;
Q1-MAR-2001
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Q1-JUN-2002
                                                                                                                                                                                                                                                Glockner G. Szafranski K., Winckler 7
COX E., Eichinger L., Noegel A.A., Ros
"The Complex Repeats of Dictyostellium
Genome Res. 11:585-594(2001).
EMBL; AF298204; AAG37039.1;
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Eukaryota; Myc
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-AX4: TRANSPOSON-GYPSY-LIKE LTR RETROTRANSPOSON DGLT-Al; Glockner G., Szafranski K., Winckler T., Dingermann T., Quail
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InterPro; IPR000717; PCI.
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cetozoa; Dictyosteliida;
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Rosenthal A.;
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Q04373;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
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YDR496C O
                                                                                                                                                                                                   D9719.
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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food borne pathogen Campylobacter jejuni
SEQUENCE FROM N.A. Dietrich F.S., Mulligan Carpenter J., Chen E.,
                                                                                                            Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomy
Saccharomycetales; Saccharomycetaceae; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL139077; CAB73497.1;
HSSP; P06132; 1URO.
InterPro; IPR000257; Uro_decarbxyls
Pfam; PF01208; URO-D; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-NCTC 11168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Campylobacter.
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01-MAR-2002
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00906; UROD_1; 1.
PROSITE; PS00907; UROD_2; UNKNOWN_1.
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                                                                                       NCBI_TaxID=4932;
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11; Conserv
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(TrEMBLrel. 15,
(TrEMBLrel. 20,
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55.0%;
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    Cherry J.M.
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Last annotation update)
ase (EC 4.1.1.37).
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Last annotation updat
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  E., Araujo
., Chung E.,
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      R., Aviles
, Duncan M.
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01-MAY-1999
01-DEC-2001
Slime mold (
                                                                                                                                                                                                                                                                                                                                                                                                                                                        096849
096849;
                                                                                                MEDLINE=86079481; PubMed=2416457; Cappello J., Handelsman K., Lodish H.F.; "Sequence of Dictyostelium DRS-1: An apparent retrotransposon with inverted terminal repeats and an internal circle junction sequence.
                                                                                                                                                                                                     MEDLINE=85085937; PubMed=6096693;
Cohen S.M., Cappello J., Lodish H
"Transcription of Dictyostelium d
                                 RNA-directed DNA p
SEQUENCE 608 AA;
                                                                             Cell 43:105-115(1985).
EMBL; M11339; AAA33195.1; -.
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                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
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                                                        Pfam; PF00078; rvt; 1.
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Submitted (JUN-1997) to tl
EMBL; U33057; AAB64938.1;
SGD; S0002904; YDR496C.
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                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=44689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001313; Pumili
Pfam; PF00806; PUF; 4.
SMART; SM00025; Pumilio; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1995)
                                                                    [nterPro
                                                                                                                                                                                                                                                                                          'Dictyostelium transposable element
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 Similarity
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                                                                 IPR000477;
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                                 polymerase.
A; 70317 MW;
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Dictyostelium discoideum
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47.6%;
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Pred.
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Pred. No. 58;
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48.5;
No. 63;
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                                   CRC64;
          Length 608;
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SMART; SM00230; CYSPC; 1.
SMART; SM00054; EFh; 3.
PROSITE; PS00018; EE_HAND; UNKNOWN_1.
PROSITE; PS00139; THIOL_PROTEASE_CYS;
                                              Pfam; PF01067; Calpain_III; 1
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2;
PRINTS; PR00704; CALPAIN.
                                                                                               InterPro; IPR002048;
InterPro; IPR001300;
InterPro; IPR000169;
                                                                                                                                  Biochem. Biophys. F
EMBL; AF261089; AAF
HSSP; P04574; IALV.
                                                                                                                                                  "cDNA cloning by amplification of circularized fir reveals non-IRE-regulated iron-responsive mRNAs"; Biochem. Biophys. Res. Commun. 275:223-227(2000). EMBL; AF261089; AAF99682.1; .
                                                                                                                                                                                                            TISSUE=BRAIN ASTROCYTOMA; MEDLINE=20403900; PubMed=
                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cappello J., Handelsman K., Lodish H.F.;
"Sequence of Dictyostellum DIRS-1: an apparent retrotransposon inverted terminal repeats and an internal circle junction seque Cell 43:105-115(1985).

EMBL; M11340; AAA70202.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                          Calpain large polypeptide L2.
                                                                                                                                                                                                                                                                                                                                                          Q9нвв1;
                                                                                                                                                                                                                                                                                                                                                                        Q9HBB1
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MEDLINE=86079481; PubMed=2416457;
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                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000477; RVTse.
Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=44689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical 70.4 kDa protein.
Dictyostelium discoideum (Slime mold).
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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512 QWKQCLAFPPPILLPSILEKM
                                                                                                                                                                                               Connor J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KWKKLLKKPPP-LLKKLLKKL 20 | | | | | | | | | | | | | |
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| QWKQCLAFPPPILLPSILEKM 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein; RNA-directed DNA polymerase.
608 AA; 70376 MW; B7285DAB3FE2FBF3 CRC64;
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                                                                                                                                                                                                             PubMed=10944468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.2%;
47.6%;
                                                                                                SHprot_acsite
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                                                                                                                         EF-hand
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Pred. No. 6
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RESULT 13
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QBWU26
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Best Local
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Q8WU26;
Q1-MAR-2002 (TrEMBLrel. 20, Crea
Q1-MAR-2002 (TrEMBLrel. 20, Last
Q1-JUN-2002 (TrEMBLrel. 21, Last
Hypothetical 80.0 kDa protein.
                  "Calpain isoforms in the eye of monkey.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF284441; AAG22771.1; -.
HISSP; P04574; IALV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9GLG1;
                                                                                                                                                                                                                           Cercopithecinae;
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC021303; AAH21303.1; ... InterPro; IPR0013048; EF hand. InterPro; IPR001300; Protease_C2. InterPro; IPR001309; SHprot_acsite. Pfam; PF01067; Calpain_III; 1. Pfam; PF01068; Peptidase_C2; 1.
                                                                                                                                                TISSUE-RETINA;
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           Calpain 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 700 AA; 80009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00704; CALPAIN.
SMART; SM00230; CysPc; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_2.
PROSITE; PS00139; THIOL_PROTEASE_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JAN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
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C02.002;
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16,
21,
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Pred. No. 72;
5; Mismatches
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Pred. No. 72;
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R InterPro; IPR001300; Protease_C2.
R InterPro; IPR00169; SHprot_acsite.
Pfam; Pf00067; Calpain_III; 1.

DR Pfam; PF00036; efhand; 3.

DR Pfam; PF00036; eppidase_C2; 1.

DR PINTS; PR00704; CALPAIN.

DR SMART; SM00230; CysPc; 1.

DR SMART; SM00230; CysPc; 1.

DR PROSITE; PS00018; EFh; 3.

DR PROSITE; PS00018; DR PROTEASE_CYS; 1.

PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00139; THOOL_PROTEASE_CYS; 1.

The PROSITE; PS00139; THOOL_PROTEASE_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
Q9YGC1
                                                                                                     Query Match
Best Local S
Matches 8
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Q9YGC1;
O1-MAY-1999 (TIEMBLIEL 10, C:
O1-MAY-1999 (TIEMBLIEL 10, L:
O1-MAR-2002 (TIEMBLIEL 20, L:
B cell linker protein BLNK.
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SEQUENCE FROM N.A.
MEDLINE-99146381; PubMed-10023776;
Ishiai M., Kurosaki M., Pappu R., Okawa K., R.
Shibata M., Iwamatsu A., Chan A.C., Kurosaki
Shibata M., Iwamatsu A., Chan B.C., Kurosaki
                                                                                                                                                                                                                                                                                                                                                                                                                            "BASH, a novel signaling molecule of the bursa of Fabricius.",
J. Immunol. 161:5804-5808(1998).
EMBL; AF089727; ADD12783.1; -
EMBL; AB015289; BAA36275.1; -
HSSP; P08487; 2PLD.
                                                                                                                                                                                                        PROSITE; PS50001; SH2; SEQUENCE 552 AA; 61
                                                                                                                                                                                                                                                PRINTS; PRO1217; PRICHEXTENSN.
PRINTS; PRO0401; SH2DOMAIN.
PRODOM; PD000093; SH2; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002965; P_rich_extensn.
InterPro; IPR000980; SH2.
Pfam; PF00017; SH2; 1.
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Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goitsuka R., Fujimura Y., Mamada H., Umeda A., Morimura Uetsuka K., Doi K., Tsuji S., Kitamura D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99049801; PubMed=9834055;
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8; Conserv
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10; Conserv
WDRLKKKPPPSLPR 68
                                                WKKLLKKPPPLLKK 15
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5; Mismatches
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Pred. No. 72;
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RESULT 15
Q9PKS5
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Search completed: June 6, 2003, 13:24:54
Job time: 24.5 secs
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Matches 9
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InterPro; IPR00359; AAA_ATPase_centr.
InterPro; IPR001270; Chaprnin_clpA/B.
InterPro; IPR004176; Clp_N.
Pfam; PF00004; AAA; 1.
Pfam; PF00004; AAA; 1.
Pfam; PF008661; Clp_N; 2.
PRAUTS; PR00309; CLPPROTEASEA.
SMART; SM00382; AAA; 1.
PROSITE; PS00870; CLPAB_1; 1.
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Q9PKS5;
01-OCT-2000 (TTEMBLrel. 15, Created)
01-OCT-2000 (TTEMBLrel. 15, Last sequence update)
01-JUN-2002 (TTEMBLrel. 21, Last annotation update)
ATP-dependent Clp protease, subunit B.
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STRAIN=MODN / NIGG;
STRAIN=MODN / NIGG;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Salzberg S.L.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID-83560;
                                                                                                                                                                                                                                                                                                                          PROSITE; PS00870; CLPAB_1; 1.
Complete proteome.
SEQUENCE 867 AA; 96603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AE002306; AAF39246.1;
TIGR; TC0389; T.
                                                                                                          2 WKKLLKKPPPLLKKLLKKL 20
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124 WRKTVKTSPEALKELLIKL 142
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Total number of hits satisfying chosen parameters:
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RESULT 2
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ID Y107_NPVAC
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InterPro; IPR000717; PCI.
Pfam; PF01399; PINT; 1.
SMART; SM00088; PINT; 1.
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SEQUENCE 900 AA; 102989 MW;
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O49160;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable eukaryotic translation initiation factor 3 subunit 8 (eIF3 pl10) (pl05).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99065153; PubMed-9849901;
Karniol B., Yahalom A., Kwok S., Chamovitz D.A.;
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215 WEKMLSKKDKLLEKLMNK
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9; Conserv
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MW; 3C03FEDBF59AB5D1 CRC64;
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BIOB_BUCAI
BIOB_BUCAI
DDX6_XENLA
DDX6_HUMAN
DDX6_HUMAN
TP6B_PYRAB
GIDA_MYCGE
YCF0_MARPO
KZ_DROME
Y173_HUMAN
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                  PRT;
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P37610
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Match Query

Length DB

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48

Y107\_NPVAC KPB2\_RABIT CAN2\_HUMAN

score g Pred. No.

YKQO\_CAEEL YYR, PYRHO NIFX\_FRAND DCUP\_PASMU DCUP\_PASMU DCUP\_PASMU CC4\_YEAST ACE\_RABIT YZ93\_MYCGE MDM2\_MOUSE MDM2\_HONSE CAS\_SCHPO IMEI\_YERPO IMEI\_YERP

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CAN2\_RAT YP16\_METTM

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Scoring table:

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US-10-081-418-2 105

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01-NOV-1995 (Rel. 32, Las
01-NOV-1997 (Rel. 35, Las
01-NOV-1997 (Rel. 35, Las
Hypothetical 12.5 kDa pro
Autographa californica nu
Viruses; dsnAv viruses, r
Nucleopolyhedrovitus
                                                                                                                                             Subunit and mapping of the gene to Apizza processis.";
X-linked liver glycogenosis.";
Proc. Natl. Acad. Sci. U.S.A. 89:2096-2100(1992).
Proc. Natl. Acad. Sci. U.S.A. 89:2096-2100(1992).
-i- FUNCTION: PHOSPHORYLASE B KINASE CATALYZES THE PROCESSION PROSPROVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p46018;

01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Phosphorylase B kinase alpha regulatory chain,

(Phosphorylase Kinase alpha L subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C6;
MEDLINE-94303173; PubMed-8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres m.D. Bound S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., E
Ayres M.D., Howard M.D., How
                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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Virology 202:586-605(1994).
-i- SIMILARITY: TO CORRESPONDING
ACMNPV ARE FOUND AS A SINGLE
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Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                          MEDLINE=92196064;
                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=46015;
                                                                                                                                                                                                                                                          "cDNA cloning of a liver isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
ENZYME REGULATION: BY PHOSPHORY AND BY CALCIUM.

PATHWAY: Glycogen metabolism. SUBUNIT: POLYMER OF 16 CHAINS, AND DELTA. ALPHA AND BETA ARE FORTHLYTIC CHAIN, AND DELTA IS COMMENTALIZED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no rest
                                                                                                                              CHAIN MAY BIND CALMODULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L22858; AAA66737.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKLLKKPPPLLKKLLKK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCLLPAPPPQLRKLEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                    PubMed=1372435;
zelik T., Hamach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12547 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update;
Last annotation update)
protein in HB65-PK2 intergenic region.
a nuclear polyhedrosis virus (ACMNPV)
s, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                            BY PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                    Hamacher C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27B17C9DB21204FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                    of the to xp22.
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    REGULATORY
CALMODULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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                                                                                                                                                                                                                                    phosphorylase kinase alpha .2-p22.1, the region of hum
                                                                                                                                                                                                                                                                                                      Willems
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                        CHAINS, G
                                                                                                            VARIOUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver
                                                                                                                                                                                                                                                                                                    P.J.,
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                                                                                                                                                    PHOSPHORYLATION
IN I. THE ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      γd
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a nuclear
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                          GAMMA IS
                                                                                                            SERINE
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                                                BETA,
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                                                GAMMA
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                                                                                                                                                                                                                                        human
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RESULT 4
CAN2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               P17655; Q16738;
01-AUG-1990 (Rel. 1
01-AUG-1990 (Rel. 1
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                          P17655; Q16/30,
O1-AUG-1990 (Rel. 15, Created)
O1-AUG-1990 (Rel. 15, Last sequence update)
O1-JUN-2002 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precursor
"The crystal structure of calcium-free human m-calpain sugges electrostatic switch mechanism for activation by calcium.", proc. Natl. Acad. Sci. U.S.A. 97:588-592(2000).
-i- FUNCTION: Calcium-regulated non-lysosomal thiol-protease catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
                                                                                                                                                                                                                                                      "Molecular cloning of the cDNA for high-Ca2+-requiring form of human C Biochemistry 27:8122-8128(1988).
                                                                                                                                                                                                                                                                                                    MEDLINE-89166474; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced th between the Swiss Institute of Bioinformatics and t the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                  (Calcium-activated ne (Millimolar-calpain). CAPN2 OR CANPL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
                                                                                                         MEDLINE-20105516;
                                                                                                                                                          dependent
                                                                                                                                                                                                                                                                                         Suzuki K.;
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X60421; CAA42952.1;
                                                                          Suzuki K., Bode W.;
                                                                                    Nakagawa K.,
                                                                                                Strobl
                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
                                                                                                                                                           transcription of a human dependent protease.";
                                                                                                                                                                     Hata A., Ohno S., Akita Y., Suzuki K.; "Tandemly reiterated negative enhancer-like transcription of a human gene for the large
                                                                                                                                                                                                                     TISSUE=Lymph
                                                                                                                                                                                                                                SEQUENCE OF 1-79
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAN2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED
                                                                                                                                                                                                        MEDLINE=89197947;
                                                                                                                                               Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NONMUSCLE TISSUES.
SIMILARITY: BELONGS
CHAINS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolism;
                                                                                                                                                Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLKKPPPLLKKLLKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        808 8
1059 10
1235 AA;
                                                                                  105516; PubMed=10639123; Fernandez-Catalan C., Braun M., Irie A., Sorimachi H., Bouren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                264:6404-6411(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1099
                                                                                                                                                                                                                                                                                                     PubMed=2852952;
., Ohno S., Emori
                                                                                                                                                                                                          PubMed=2539381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 838
                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.78;
56.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CALMODULIN-BINDING CALMODULIN-BINDING MW; B8E218C1D8C6F37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLASE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                     Ca2+-activated
                                                                                                                                                                                                                                                                                the
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                                                                                     Bourenkow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
20;
                                                                                                                                                                                                                                                                                large subunit
                                                                                                                                                                                                                                                                                                        Kawasaki H.,
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                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
                                                                                  Huber R.,
kow G., Bar
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                                                                                                                                                                        subunit
                                                                                                                                                                                   elements
                                                                                                                                                                                                                                                                                                                                                                                                                           [ (EC 3.4.22.17)
  (M-type) (M-calpain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINASE
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                                                alpain suggests calcium.";
                                                                                                                                                                                                                                                                      neutral
                                                                                      Bartunik
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                                                                                                                                                                        s regulate
of calcium-
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                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                     Masumoto I
                                                                                                                                                                                                                                                                                  of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
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                                                                                         Query Match
Best Local S
Matches 10
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InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsit
Pfam; PF00036; efhand; 3.
Pfam; PF00036; Peptidase_C2; 1.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF01067; Calpain_III; 1.
PRINTS; PR00704; CALPAIN.
PRODOM; PP000012; EF-hand; 1.
SMART; SM00230; CysPc; 1.
SMART; SM00230; CysPc; 1.
SMART; SM00230; EF_HAND; 2.
PROSITE; PS00018; EF_HAND; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M23254; AAA35645.1; -
EMBL; J04700; AAA55760.1; -
PIR; A31218; A31218.
PDB; 1KFU; 07-DEC-01.
MEROPS; C02.002; -
Genew; HGNC:1479; CAPN2.
                                                                                                                                            CA_BIND
CA_BIND
CA_BIND
DOMAIN
DOMAIN
ACT_SITE
                                                                                       CONFLICT
SEQUENCE
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DOMAIN
                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                               PROSITE; PRO00139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.

Hvdrolase; Thiol protease; Calcium-binding; Repeat; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                             CONFLICT
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 114230;
                                                                                                                                                                                                                                                                                     ROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING [
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Arg-|-Xaa with Leu or Val as the P2 residue.

COEACTOR: Blinds 3 calcium ions.

ENZYME REGULATION: Activated by 200-1000 micromolar concentration of calcium and inhibited by calpastatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Heterodimer of a large (catalytic) and
 213
                                             10;
                                                      Similarity
             KWKKLLKKPPPLLKKLLKK
EWYE-LKKPPPNLFKIIQK
                                                                                       700
                                           Conservative
                                                                                                   ξ
                                                                                                   80006
                                                    46.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease_C2
                                                                                       Œ,
                                                                                 ANCESTRAL CALCIUM SITE 4 (E
ANCESTRAL CALCIUM SITE 4 (E
BY SIMILARITY.
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BY SIMILARITY.
S -> G (IN REF. 2).
MR -> IE (IN REF. 2).
MR -> 1E (IN REF. 2).
MR -> A944Dl3BC846553l CRC64;
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Pred.
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DOMAIN IV.
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EF-HAND 2.
EF-HAND 3.
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Mismatches
                                                                48.5;
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                                                              Length 700;
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SUBUNIT.
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RESULT 5 V226\_FOWPV

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Best Local S
Matches 8
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=99120557; PubMed=9923682;

MEDLINE=99120557; PubMed=9923682;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig r.

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carnel G.,

Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,

Tummino P.J., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis
                                                                                                                                                                       Q9ZLM8;
16-OCT-2001
16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V226_FOWPV
Q9J509;
16-OCT-2001
16-OCT-2001
16-OCT-2001
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BINDING
ACT_SITE
                                                                                                                                                                                                                                HELPJ
                                                                                                                                                    HEME OR JHP0551.
                                                                                                                                                                                                                                                                                                                                                                                                                              PRODOM: PD000001; EUK_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Afonso C.L., Tulman E.R., Lu Z., "The genome of fowlpox virus."; J. Virol. 74:3815-3831(2000).
                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                        Helicobacter pylori J99
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=20193820; PubMed=10729156;
                                                                                                        NCBI_TaxID=85963;
                                                                                                                                                                                                                   DCUP_HELPJ
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POXVIRUSES SUBFAMILY.
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IPR002290; Ser_thr_pkinase.
                                                                                                                                                   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat
Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40,
(Rel. 40,
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14 292 PROTEIN KINASE.
20 28 ATP (BY SIMILARITY).
43 43 ATP (BY SIMILARITY).
147 BY SIMILARITY.
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a; epsilon subdivision; Helicobacter group;
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4.1.1.37)
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Best Local
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                                                                                                                                                                                                                                                                                                                                      MEDLINE-97394467; PubMed-9252185;

Mond J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.

Relson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.

Cotton M.D., Weldman J.M., Fujil C., Bowman C., Watthey L., Wallin

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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Nature 397:176-180(1999)
-1- CATALYTIC ACTIVITY: Uroporphyrinogen-III = copropo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97394467; PubMed=97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uroporphyrinogen decarboxylase HEME OR HP0604.
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15-JUL-1998 (Rel. 36,
16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001487; AAD06123.1; -.
HSSP; P06132; 1URO.
InterPro; IPR000257; Uro_decarbxyls
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between the
the European
                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                       pylori.";
Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                   Cotton M.D., Weidman J. Hayes W.S., Borodovsky Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori (Campylobacter Bacteria; Proteobacteria; epsilon :
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SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE UROPORPHYRINGEN DECARBOXYLASE FAMILY.
                                                                                                    PATHWAY: PORPHYRIN biosynthesis, SUBCELLULAR LOCATION: Cytoplasmic (Probable). SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.
                                                                                                                                                                                                              CATALYTIC
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CE 339 AA; 38367 MW; 1
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     Swiss Institut
Bioinformatics
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                                                                                                                                                                                                                                                                                       genome sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
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KI67_HUMAN
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16-OCT-2001
the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00906; UROD_1; 1.

PROSITE; PS00907; UROD_2; 1.

Lyase; Decarboxylase; Porphyrin biosynthesis; Complete proteome.

SEQUENCE 339 AA; 38339 MW; 766E03ADAAF42726 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000257; UPF Pfam; PF01208; URO-D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=94043435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P46013;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Cell Biol, 123:513-522(1993).
                                                                                                                                                   ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. DEVELOPMENTAL STAGE: EXPRESSION OF THIS ANTIGEN OCCURS PREFERENTIALLY DURING LATE G1, S, G2, AND M PHASES OF THE CYCLE, WHILE IN CELLS IN G0 PHASE THE ANTIGEN CANNOT BE DECYCLE, WHILE IN CELLS IN G0 PHASE THE ANTIGEN CANNOT BE DECYCLE.
                                                                                                                                                                                                                                                      SÜBCELLULAR LOCATION: NUCLEAR. PREDOMINANTLY LOCALIZED PHASES IN THE PERINUCLEOLAR REGION, IN THE LATER PHASES DETECTED THROUGHOUT THE NUCLEAR INTERIOR, BEING PREDOMI LOCALIZED IN THE NUCLEAR MATRIX. IN MITOSIS, IT IS PRES
                                                                                                                                      SIMILARITY: CONTAINS 1 FHA DOMAIN.
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PROLIFERATION
                                                                                                                                                                                                                                       CHROMOSOMES
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                                                                                                     SWISS-PROT entry is copyright.
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annotation
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Pred. No.
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Matches 9
                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 814-822.

X MEDLINE-90016865; PubMed-2798129,

A Brault V., Hibrand L., Candresse T., le Gall O., Dunez

"Nucleotide sequence and genetic organization of Hunga:
chrome mosaic nepovirus RNA2.";

Nucleic Acids Res. 17:7809-7823(1989).

-i- FUNCTION: THE PROTEIN LOCATED AT THE N-TERMINAL END
NEPOVIRUS POLYPROTEIN COULD BE REQUIRED FOR NEMATOD
OF THE VIRUS.
                                                                                                                                                                                                                   POLZ_GCMV STANDARD,
P13026;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MIM; 176741;

InterPro; IPRO00253; FHA_domain.

Pfam; PF00498; FHA; 1.

SMART; SM00240; FHA; 1.

PROSITE; PS50006; FHA_DOMAIN; 1.
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Viruses; ssRNA positive-strand
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                                           PTM: THE RNA2 POLYPROTEIN IS CLEAVED BY AN RNA1-ENCODED PROTI
TO YIELD THE MATURE COAT PROTEIN AND AN 84 kDa PROTEIN WHICH
FURTHER CLEAVED INTO TWO PRODUCTS OF APPROXIMATELY 46 AND 48
SIMILARITY: TO THE RNA2 POLYPROTEIN OF OTHER NEPOVIRUSES.
       SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on if
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cycle;
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27 76 FHA.
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Pred. No.
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Hungarian
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Matches 9
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Mitogen-activated protein kinase 14A (EC 2.7.1.-) (MI (D38 MAPK) (D938) (D-p38a).

(D38 MAPK) (D938) (D-p38a).

MPK2 OR P38A OR CG5475.

Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrusi Eukaryota; Metazoa; Arthropoda; Endopterygota; Diptera, Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBL_TaxID-7227;
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InterPro; IPR005054; Nepo_coat.
InterPro; IPR005305; Nepo_coat_C.
InterPro; IPR005306; Nepo_coat_N.
Pfam; PF03391; Nepo_coat; 1.
Pfam; PF03688; Nepo_coat_C; 1.
Pfam; PF03689; Nepo_coat_N; 1.
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle George R.A., Lewis S.E., Richards S. D., Zhang Q., Chen L.X. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiff Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M14A_DROME
062618; 046
                                                                                                                        STRAIN=Berkeley;
MEDLINE=20196006;
                                                                                                                                                                                                            "Molecular cloning and characterization activated protein kinase.";
J. Biol. Chem. 273:369-374(1998).
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SEQUENCE
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MEDLINE=98252940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z.S.,
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11 1324
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                                                                                                                                                                                                                                                                        PubMed=9417090; .-Y., Brey P.T.,
                                                                                                                            PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9584193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1006
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COAT PROTEIN.
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A., Galle R.F.,
, Henderson S.N.,
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RA Dodson K., Doug L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guah P., Harris M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guah P., Harris M. A., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C., Alaish P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K. RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K. RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb JM., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb JM., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G. RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Syler E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Yeinston S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.G. RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.G. RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.G. RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.G. Ra Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.G. Ra Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.G. Ra Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.G. Ra Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.G. Ra Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.G. Ra Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.G. Ra Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.G. Ra 
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Beeson K.Y.,
                                               HSSP; Q16539; IMFC:
Flybase; FBgn0015765; Mpk2.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003527; MAP_kin.
InterPro; IPR003527; MAP_kin.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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the Euro
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Ballew R.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities
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Proc. Natl. Acad. Sci. U.S.A.
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MEDLINE=92335284; PubMed=1378625;
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SUBCELLULAR LOCATION: NUClear.
DEVELOPMENTAL STAGE: Expressed both mate
Levels are highest at the preblastoderm
present throughout development.
SIMILARITY: BELONGS TO THE SER/THR FAMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through meen the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
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FUNCTION: Kinase involved in a signal transduction properties of the second section of the second seco
                                                                                                                                                                                                                                                        AF035546; AAC39030.1; -. AF035547; AAC39031.1; -. U86867; AAB97138.1; -. AE003746; AAF56244.1; -.
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Best Local
                                              entities
or send a
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01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Inner coat prote
Core shell protein P30; Nucleoprotein P10].
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                                                                                                                                                            POLYPROTEIN.
-!- SIMILARITY: CONTAINS 1 CCHC-TYPE ZINC FINGER.
-!- CAUTION: REE. 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY.
                                                                                                                                                                                                                                     gag-pol region.";
J. Virol. 47:137-145(1983).
-i- PTM: SPECIFIC ENXYMATIC CLEAVAGES IN VIVO YIELD
-i- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A
                                                                                                                                                                                                                                                                                                                                                                                                                            Kato S., Matsuo K., Nishimura N., Takahashi
"The entire nucleotide sequence of baboon en
chimeric genome structure of murine type C a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=83241915;
                                                                                                                                                                                                                                                                                                                                                                                                                retroviruses."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baboon endogenous virus (strain M7).
Viruses; Retroid viruses; Retroviridae; Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAG_BAEVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                    modified and this statement
                                                                                                                                                                                                                                                                                                               "Provirus of M7
                                                                                                                                                                                                                                                                                                                               Tamura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=11764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P03341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 KWKELIYKEVTNFKPPPSYAQVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KWKKLLK-----KPPPLLKKLLK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
25
31
54
E 154
E 184
186
186
77
                                                s requires a license agreement (San email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P10268;
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PS00107;
PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00108;
                                                                                                non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                             baboon endogenous virus: nucleotide
                                                                                                                                                                                                                                                                                                                                                 PubMed=6408267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN_KINASE_DOM; PROTEIN_KINASE_ST; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAPK; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39
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PHOSPHORYLATION (
PHOSPHORYLATION.

D -> G (IN REF. 2

K -> R (IN REF. 2

L -> A (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB
Pred. No. 16;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B3592B869F97990E CRC64;
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> R (IN REF. 4).
> A (IN REF. 2).
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SIMILARITY).
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n kinase; ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein P10].
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16;
                                                                    (See http://www.isb-sib.ch/announce/
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                                                                                                      as
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ndogenous virus
                                                                                  Usage
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                                                                                                        its content
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                                                                                                                                                                                                                                              MATURE PROTEINS GAG-POL
                                                                                                                                                                                                                                                                                                                sequence of
                                                                                                                    restrictions
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                                                                                                                                           a collaboration -
MBL outstation -
                                                                                       for
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                                                                                                                                          outstation
                                                                                      in no way commercial
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D10032; X05470;

BAA00923.1; CAA29027.1;

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RESULT 12
PPA HAEIN
ID PHEN
PA HAEIN
AC P4516
DT 01-NO
DT 15-JU
DE alan1
DE carbo
GR PACB
OX Haemo
OC Haemo
OX NCBI_
RN [1]
RP SEQUE
RA KETLA
RA FILE1E
RA Weidm
RA Weidm
RA Vente
RA Gneh
RA Fine
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RA Gren
RA Fine
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO00840; Gag_MA.
InterPro; IPRO0336; Gag_p30.
InterPro; IPRO0336; Daf_CCHC.
Pfam; PF00098; zf-CCHC; 1.
Pfam; PF01140; Gag_MA; 1.
Pfam; PF022093; Gag_M3; 1.
SMART; SM00343; ZnF_CCHC; 1.
PROSITE; PS50158; ZF_CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                          Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last annotation update)
Penicillin-binding protein 4 precursor (PBP-4) [Includes: D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) (DD-peptidase) (DD-carboxypeptidase); D-alanyl-D-alanine-endopeptidase (EC 3.4.99.-) (DD-carboxypeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Penicillin-binding protein 4 precursor (PBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PBP4_HAEIN
P45161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
ZN_FING
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAEIN
                                                                                                                                                                                                                                                                                                             Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DACB OR HI1330
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Zinc-finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
PIR; ;
PIR; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                    CATALYTIC ACTIVITY: D-alanyl-D-alanine + H(2)O = PATHWAY: FIRML STRAGES IN PEPTIDOGLYCAN SYMTHESIS: SUBCELLULAR LOCATION: Periplasmic (Potential). SIMILARITY: BELONGS TO PEPTIDASE FAMILY $13; ALSO D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 3 FAMILY.
                                                                                                                                                                                            FUNCTION: NOT INVOLVED IN TRANSPEPTIDATION BUT EXCLUSIVELY CATALYSES A DD-CARBOXYPEPTIDASE AND DD-ENDOPEPTIDASE REACT (BY SIMILARITY)
SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JT0260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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226
477
537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma subdivision; Pasteurellaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORE PROTEIN P15.
CORE SHELL PROTEIN P30.
NUCLEOPROTEIN P10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB
Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCHC-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INNER COAT PROTEIN P12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5DEEE4437CFCFB79 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clayton R.A., Kirkness E.F., Dougherty B.A., Merrick J.M., elds C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DΒ
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                                                                                                 ALSO KNOWN
                                                                                                                                                                        N
                                                                                                                                                                     D-alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DD-
C 3.4.99.-) (DD-
                                                                                                                                                                                                                   REACTION
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RESULT 13
CAN2_MM
CAN2_MM
AC 008529
DT 01-NOV
DT 16-OCT
DT 15-UN
DE CAlpai
DE (Milli
GN CAPN2.
OS MUS mu
OC EMMANAI
OX MCBLT
RN [1]
RP SEQUEN
RC STRAIN
RA Dear N
RT Genomi
RL Genomi
RL Genomi
RL STRAIN
RA DEAL
RY SEQUEN
RC STRAIN
RA DEAL
RY SEQUEN
RC STRAIN
RA DEAL
RY SEQUEN
RC STRAIN
RA Glass
RT SUBMitt
RN [3]
RP SEQUEN
RC TISSUE
RA Glass
RT SUBMITT
CC -1- FT
CC
CC -1- GA
CC -1- CA
CC -1- CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
    CAN2_MOUSE STANDARD; PRT; 700 AA.

008529; 035518; 054843;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)
(Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)
(Millmolar-calpain) (80 kDa M-calpain subunit) (CALP80).
                                                                                                                                                                                                                                                                      Dear N., Matena K., Vingron M., Boehm T.;
"A new subfamily of vertebrate calpains lack
domain: implications for calpain regulation
Genomics 45:175-184(1997).
                                                                                                                                                         TISSUE-CNS;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                    Submitted (OCT-1997)
                                                                                                                                                                                                                     Ozaki Y
                                                                                                                                                                                                                                STRAIN=BALB/c;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                MEDLINE-97480729; PubMed-9339374;
                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00922; PRP4; 1.
TIGRFAMS; TIGR00666; PBP4; 1.
TIGRFAMS; TIGR00666; PBP4; 1.
TigrFAMS; Tigr009666; PBP4; 1.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32812; AAC22975.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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479 į
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistance; Periplasmic; Com
26 POTENTIAL.
27 479 PENICILLIN
69 69 ACYLATED B
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                                                                                                                                                                                              EMBL/GenBank/DDBJ databases.
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Pred. No. 25;
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ACYLATED BY PENICILLIN (FORMS PART OF
THE ACTIVE-SITE CLEFT) (BY SIMILARITY).
SUBSTRATE-BINDING (BY SIMILARITY).
632868C61206CB48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                               lacking a calmodulin-like tion and evolution.";
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                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                    Murinae;
                                                                similarity).
          concentrations
                                                   Met-|-Xaa
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Best Local
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CAN2_RAT

Q07009;

01-JUN-1994

01-JUN-1994

15-JUN-2002

Calpain 2, 18
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CA_BIND
CA_BIND
CA_BIND
DOMAIN
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ACT_SITE
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CONFLICT
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DOMAIN
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ART; SMO0230; CysPC; 1.

ART; SMO0230; ESPH; 2.

ART; SMO0230; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_LIS; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.

ARCHORS TO THE SMALL SUBUNIT (POT ANCHORS TO THE SMALL SUBUNIT (POT CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (POT CALPAIN 3, LARGE [CATALYTIC] SUBUNIT (POT CALPAIN 4)

ART: SMO0230; CysPC; 1.

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DOMAIN
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InterPro; IPR0012048; Er-hand.
InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam: PF00648; Peptidase_C2; 1.
Pfam: PF01067; Calpain_II; 1.
PRINTS; PR00704; CALPAIN.
ProDom; PD000012; EF-hand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS;
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                                                                                                                                                                                                                                                                                                                      SEQUENCE
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(regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
subcrane upon Ca++ binding.
Translocates
SEF-HAND CALCIUM-BINDING
Translocates
FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y10139; CAA71227.1; -. D38117; BAA22964.1; -.
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9; Conser
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(Rel. 41, Last annotation updat
large [catalytic] subunit precur
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                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                            WW;
                                                                                                                                                                                                                                                   ; Score 45.5; D; Pred. No. 36; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                     LINKER.

DOMAIN IV.
EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
EF-HAND 3.
ANCESTRAL CALCIUM SANCESTRAL CALCIUM SANCESTRAL RITY.
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                                                                                              PRT;
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         precursor
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UBUNIT (POTENTIAL).
LYTIC] SUBUNIT.
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Moldoveanu T., Ho:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUTAGENESIS OF CYS-105; HIS-262; ASN MEDLINE=95361909; PubMed=7635186; MEDLINE=95361909; PubMed=7635186; Arthur J.S.; Gauthier S., Elce J.S.; "Active site residues in m-calpain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Calpain mutants with increased Ca2+
the role of the C(2)-like domain.";
J. Biol. Chem. 276:7404-7407(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Ca(2+)-induced structural changes in partial proteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys.
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"Molecular cloning and bacterial II 80 kDa subunit.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-94032492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ca(2+)-dependent protease activation.";
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Hosfield C.M., Eld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21269273; PubMed=11102442;
Hosfield C.M., Moldoveanu T., Davies P.L.,
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(Millimolar-calpain).
                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE-20059310; FL... Davies P.L., Jia Z.;
Hosfield C.M., Elce J.S., Davies P.L., Jia Z.;
"Crystal structure of calpain reveals the structural mode of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett.
                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE=20069318; PubMed=10601010;
                                                                                                                                      EMBL; L09120; AAA16327.1;
                                                                                                                                                                                    or send an
                                                                                                                                                                                                          modified and this statement entities requires a license
                                                                      MEROPS;
                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 kDa subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Calcium-regulated non-lysosomal thiol-protease catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction. CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met Arg-|-Xaa with Leu or Val as the P2 residue. COFACTOR: Binds 3 calcium ions. COFACTOR: Binds 3 calcium ions.
                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                    (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of calcium and inhibited by calpastatin. SUBUNIT: Heterodimer of a large (catalytic) and
                                                                                       S38361; S38361.
1DF0; 21-JUN-00
                                                                      C02.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18:6880-6889(1999)
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                     IPR002048;
IPR001300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368:397-400(1995).
                                                                                                                                                                                    equires a license agreement (S email to license@isb-sib.ch).
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es P.L., Samis J.A.,
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SMART; SM00230; CysPc; 1. SMART; SM00054; EFh; 2. PRINTS; PR00704; CALPAIN. ProDom; PD000012; EF-hand; 1. Pfam; PF00036; efhand; 3.
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MEDLINE-90221821; PubMed-2326168;

MEDLINE-90221821; PubMed-2326168;

Bokranz M., Klein A., Meile L.;

"Complete nucleotide sequence of plasmid pME2001 of Methanobacterium thermoautotrophicum (Marburg).

Nucleic Acids Res. 18:363-363(1990).

Nucleic Acids Res. 18:363-363(1990).
                                                                                                                                                                                                                                                                                                          P14935;
Ol-APR-1990 (Rel. 14, Created)
Ol-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 16.7 kDa protein.
Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
Plasmid pME2001.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriaceae; Methanobacteriaceae; Methanobacteria.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.
PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
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ANCESTRAL CALCIUM SITE 5
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CALPAIN 2, LARGE [CATALYT
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2, LARGE [CATALYTIC] SUBUNIT.
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